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Studies of Genotype-Environment Interaction shown by Coleoptile length in Wheat (Triticum aestivum L. em Thell)

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University of Rajshahi

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Studies of Genotype–Environment Interaction shown by Coleoptile length in Wheat

(*Triticum aestivum* L. em Thell)

By

QUAZI NAZRUL ISLAM, M. Phil.

A THESIS
SUBMITTED TO THE UNIVERSITY OF RAJSHAHI
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FOR THE DEGREE OF
DOCTOR OF PHILOSOPHY

DEPARTMENT OF BOTANY
UNIVERSITY OF RAJSHAHI
BANGLADESH.

DECEMBER, 1984

DEDICATION

To the memory
Professor Ali M. Eunus
this work is respectfully
dedicated.

DECLARATION

I hereby declare that the whole of the work now submitted as a thesis for the degree of Doctor of Philosophy of the University of Rajshahi is the result of my own investigation.

(Quazi Nazrul Islam)

Candidate

(O.I. Joarder)

Supervisor

CERTIFICATE

I hereby certify that the work embodied in this study has not already been submitted as a thesis in substance for any degree, and has not been concurrently submitted in candidature for any degree.

Q.N. Islam 13/12/84
(Quazi Nazrul Islam)
Candidate

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INTRODUCTION

Wheat, like other cereal grains, has many natural advantages as a food. It is nutritious, concentrated, readily stored and transported, and easily processed to give highly refined raw foods. The products are bland, fit into countless recipes, and suit many tastes. Unlike any other plant derived food, wheat contains gluten protein which enables a leavened dough to rise by forming minute gas cells that hold carbon dioxide during fermentation. This property enables bakers to produce light bread.

Wheat provides almost 20% and rice about 21% of the total food calories for the people of the world. Rice, wheat, corn, and potatoes are the leading food staples and rank in this order of importance. Wheat is the national food staple in 43 countries. It is the main staple for one billion people or about 35% of the world's population (Brown, 1963). Dependence upon wheat varies widely with geographic regions. In Europe and the USSR over 30% of the calories come from wheat, while in most other regions less than 20% are derived from wheat.

As a food, wheat is the major ingredient in most breads, rolls, chapaties, crackers, cookies, biscuits, cakes, doughnuts, muffins, pancakes, waffles, noodles, pie crust, ice cream cones, macaroni, spaghetti, puddings, pizza, bulgur, rolled

flakes, many hot and ready-to-eat breakfast foods, and baby foods. It is a common thickener in soups, gravies, and sauces and occurs in candies and beverages. Germ, bran, and malt are additional forms of wheat products.

Livestock and poultry thrive on wheat grain as a part of the ration and feed channels utilize most of the wheat by products from flour milling. The straw may be fed as a part of the roughage for ruminants and is used extensively for livestock bedding. The green forage may be grazed by all classes of livestock and the green crop can be harvested as hay or silage.

In soil management and rotations wheat serves as a companion crop with legumes and grasses as a greem manure crop and as a cover crop to reduce erosion and suppress weeds.

In industry wheat grain is used as the source of starch for pastes, alcohol, oil, and gluten. The straw may be used for newsprint, paperboard, packing, and art objects. The ripe unthreshed heads make decorative sheaves and bouquets. The uses of wheat, then, are extensive and varied. It is impossible to list all of them.

The world's wheat acreage and production are clearly concentrated in the northern hemisphere (U.S. Department of Agriculture, 1965). The USSR has the greatest harvested

acreage of any country, but the Asian countries together (including China) have more. European countries and North America together have about the same acreage as the USSR. These three great areas encompass over 90% of the world's wheat lands. In south and southeast Asia cultivation of wheat is concentrated in central, northern and northwestern India, and in Pakistan, where rainfall averages between 20 and 40 inches per year (Pal, 1964). Very little wheat is grown in Bangladesh, Burma, Thailand and other countries of south and southeast Asia since the hot humid climate in these areas is unfavourable to good wheat production.

A few years back wheat had no place in Bangladesh as a food crop. Its importance as food crop, however, was first realised in our country after the great floods of the fifties and sixties. According to the report of wheat Task Force (BARI), the total areas of wheat cultivation and total production is as given below:

Session	Total land cultivation	Total yield
1975-76	0.12 million hectares	0.258 million ton
1978-79	0.65 million acres	0.481 million ton
1979-80	1.4 million acres	1.00 million ton
1980-81	2.2 million acres	1.50 million ton

A change in the dietary habit of our people has occured and cultivation of wheat has increased gradually. Wheat is now

established as an important food crop and occupies the second position as a staple food crop in Bangladesh.

Wheat was already an important crop when history was first recorded. So accurate information on the exact time and place of its origin is not available (Clerk, 1936). The distribution of the wild wheat and grass, believed to be the progenitors of the cultivated wheat, supports the belief that wheat originated in southwestern Asia. Some species were cultivated in Greece, Persia, Turkey and Egypt in prehistoric times while the cultivation of other species may be of more recent origin. In India, evidence from Mohen-Jo-Daro excavations indicates that wheat was cultivated more than 5,000 years ago (Pal and Alam, 1938).

The genetic origin of wheat is of interest for it is a classical example of how closely related species may be combined in nature into a polyploid series. The species of *Triticum*, the genus to which the cultivated wheat belongs, and their close relatives may be divided into diploid, tetraploid and hexaploid groups, with chromosome numbers of 2n = 14, 28 and 42 respectively. Species within the tetraploid group have apparently originated as amphidiploid from two diploid species. The hexaploid species originated from the addition of a third genome to a tetraploid species.

The most common cultivated wheat of the world is hexaploid type (2n = 42), botanically known as Triticum aestivum L. em Thell. The grain may be either hard or soft in texture, brownish-red or white in colour. While commonly called 'bread wheat' and valued for this purpose, the softer textured varieties are used for pastry, crackers, sweet goods and many other products.

Wheat plants belong to the family gramineae. The plant is errect, unbranched, herbal and annual in nature. It usually grows upto 80-140 cm. in height. The plant produces fibrous roots and the stem is smooth or hairy. The leaves are exstipulate, simple, alternate, entire, dorsiventral with parallel venation. The inflorescence is a terminal spike or head consisting of 15-25 spikelets born on zigzag axis. Flowers are bisexual, stigma feathery; anthers are three in number. Wheat is a self-pollinated crop, blooming normally starts several days after the wheat spike emerge (Leighty and Sando, 1924).

The coleoptile, or first leaf, is a hollow, cylindrical structure. It completely encloses the plumule (2 or 3 rudimentary leaves surrounding the shoot apex), except for a small opening (coleoptile pore) near the apex on the side opposite the scutellum. The first green leaves of the plumule eventually emerge through this opening.

Percival (1921) considered it the primary prophyll or a leaf sheath without a blade. He indicated that the coleoptile of wheat may be green, colourless, or pink and has little photosynthetic activity. Seedling grown in the greenhouse from crosses of plants with purple vs. green coleoptiles were found to depend on two dominant duplicate factors, designated as P_1 and P_2 (Quisenberry, 1931). Other workers have found coleoptile colour to depend on either one or two factor pairs. Classification for coleoptile colour is generally good but restricted in time.

Varieties differ in coleoptile length which is in general, positively correlated with seedling emergence. Selection of types with longer coleoptiles has resulted in increased emergence from deep sowing (Allan *et al.*, 1964). The trend toward semidwarf types has created new problems in producing satisfactory stands because coleoptile length is positively correlated with plant height. If this association is complete, the grower's choice of variety, i.e., normal vs. short stature, will be decided by the relative importance of the two problems, poor stands of short stature wheat vs. lodging and too much straw of normal height varieties.

The present investigation deals with studies of genotype-environment interactions shown by coleoptile length of wheat (*Triticum aestivum* L. em Thell). The character coleoptile length was selected for study because it can be precisely

measured and can be greatly influenced by the temperature and germinating medium. The principles of analysis will apply equally well to other quantitative characters such as height and yield.

The problems especially examined are:

(1) the proportion of the variation over environments i.e. linearly related to quantitative assessment of the environment;

(2) the advantageous of alternative methods of assessing environment;

(3) the specificity of the response of genotype to diverse environmental factors;

(4) the relative sensitivities of different components of variation to change in the environments;

(5) the degree of independence of the genetic system controlling the mean expression and sensitivity aspects of phenotype;

(6) the transmission of known degrees of linear and non-linear functions of the genotype-environment interaction among parental lines to the advanced generations derived from crosses among them;

(7) estimates of components of genetic variations were used to examine the interaction of additive and non-additive component with the environment; and

(8) inheritance of coleoptile length through single cross and diallel cross.

Genetic information on the inheritance of quantitative characters is necessary for the preparation of effective and meaningful breeding programmes on wheat for its improvement; but such information was hardly available before the 1950's. Recently a number of works on the inheritance of quantitative characters of wheat have, however, been reported by several workers (Crumpacker and Allard, 1962; Briggle, 1963; Briggle et al., 1967; Walton, 1968; Walton, 1969; Singh and Gupta, 1969; Paroda and Joshi, 1970 a,b; Hsu and Walton, 1970a, b; Walton, 1971 a,b,c; Bhatt, 1972; Walton, 1972; Sun et al., 1972; Yadav and Murty, 1976; Gill et al., 1979; Jatasra and Paroda, 1978 a,b, 1979a, 1980a,b,c; and many others). As change in environment is usually associated with the change in gene expression, studies on quantitative characters become complicated when more than one environment is involved. Study of the variations in wheat over a number of environments will entail the prediction by the breeder of its phenotypic expression under related environmental conditions. This will help the breeder to improve the crop under the expected environmental variations.

Fisher (1918) studied the genetic variance in relation to environmental effects and he was the first to provide statistical methods of partitioning the total variation into genetic and environmental components. He considered that

several genes acted simultaneously on a quantitative characters producing the total variation. He developed techniques for the detection and estimation of the average main (additive) and dominance effect of these genes even when the genes were unequal in effect and exhibited incomplete dominance. He further pointed out that non-allelic interaction (epistasis) could also be separated.

With the development of first (mean) and second degree (variance and covariance) statistics, two distinct lines developed for the measurement of gene action and interaction involved in the phenomenon of continuous variation. The first, Mather (1949), developed biometrical techniques based on mathematical models of Fisher _et al._ (1932) and he described how the main and dominance variation could be estimated in a wide variety of genetical experiments. He also elaborated the methods of estimating epistatic variation. This influenced several workers (Anderson, 1953; Anderson and Kempthorne, 1954; Kempthorne, 1954; Jinks, 1956; Hayman, 1957) to approach the equivalent general representations of gene actions and interactions. Models of epistatic systems were also described by Griffing (1950), Powers (1951), and Horner, Comstock and Robinson (1955) to detect the genetic variation present in two inbred lines and their descendant families. Anderson and Kempthorne, (1954) in particular showed that all the information about additive, dominance and digenic epistatic variation is

contained in just 6-parameters. Hayman (1958) successfully measured epistatic variation and separated additive and dominance effects from epistasis by using 3-parameter and 6-parameter models. He observed that means of families or generations were influenced by epistasis which often became as great as additive or dominance variation which might be present in the form of interaction with additive effect, with dominant effect or with both additive and dominant effects.

Another line of study was developed which used the second degree statistics (variance and covariance) for the analysis of continuous variation present in random mating groups and the diallel cross technique as a means of early generation evaluation came into existence. A diallel cross consists of all possible crosses between a number of varieties which may or may not include reciprocal crosses and selfed parents (Gilbert, 1958).

Fisher introduced the mathematical model of diallel crossing system in 1918. One year later the method of diallel crossing or method of complete intercrossing as a means of comparing the breeding values of parents was stated by Schimidt, (1919). The method of analysis of diallel cross progenies was elaborated by Fisher, Immer and Tedin (1932) and later on it was further developed by Jinks and Hayman (1953), Jinks (1954) and Hayman (1954b). In 1945 Hull considered some aspects of diallel crosses. Yates (1947) described the

estimation of the additive main effect of parents and their interactions in the individual crosses from an incomplete diallel cross. The two terms "general combining ability" (GCA) and "specific combining ability" (SCA) were originally defined by Sprague and Tatum (1942). GCA and SCA refer respectively to the additive main effects of the parents and their interactions in the individual crosses.

Since then, using modern statistics in the analysis of diallel crosses, many models and techniques have been developed by a number of persons (Hayman, 1954 a,b, 1957, 1958, 1960; Jinks, 1954, 1956; Griffing, 1956 a,b; Kempthorne, 1956; Gardner and Eberhart, 1966; etc.) to apply the diallel crossing successfully to a wide field of practical purposes in plant and animal breeding. Sprague and Tatum (1942), Henderson (1948, 1952), Griffing (1950, 1956a,b), and Matzinger, Sprague and Cockerham (1959) have shown the utility of diallel crosses in the investigation of GCA and SCA. Its application to practical purposes in the early generation evaluation of parental material in breeding programmes has been discussed by Jinks (1955), Allard (1956 a,b,c), and Whitehouse, Thompson and Valle Ribeiro (1958). Rajas and Sprague (1952), Matzinger and Kempthorne (1956), and Matzinger, Sprague and Cockerham (1959), have also considered its application to the investigation of genotype-environment interaction. Some recent papers (Kempthorne and Curnow, 1961; Fyfe and Gilbert, 1963; Curnow, 1963; and Hinkelmann and

Kempthorne, 1963) have shown that the preferable method is to include in the diallel analysis only a sample of all possible crosses among a large number of parents rather than to include all possible crosses with reciprocals and selfings among a smaller number of parents.

Diallel technique has been recently used by Paroda and Joshi (1970 a,b). Tandon _et al_. (1970), Sharma and Singh (1976), Yadav and Murty (1976), Jatasra and Paroda (1978 a, 1979 a, 1980 a,b,c), Joarder _et al_. (1982) and many others in metric characters of wheat.

The relative performance of different genotypes vary under different environments indicating the existence of genotype-environment interaction. In other words, the failure of a genotype to give the same phenotypic performances when grown under different environments is the reflection of genotype-environment interaction.

The occurence of genotype-environment interaction has long provided a major challenge to obtaining a fuller understanding of the genetic control of variability. The study of genotype-environment interaction in its biometrical aspect is thus important not only from genetical and evolutionary points of view, but also very relevant to the production problem of agriculture in general and to plant breeding in particular (Breese, 1969). A knowledge of the nature and relative

magnitudes of the various types of genotype-environment interactions is important in making decisions concerning breeding methods, selection programmes and testing procedures in crops. The phenomenon has been recognised by a number of persons (Yates and Cochran, 1938; Finlay and Wilkinson, 1963; Rowe and Andrew, 1964; Eberhart and Russel, 1966; Perkins and Jinks, 1968a; Breese, 1969; Baker, 1969, and Verma and Gill, 1975).

Recently three regression approaches have been used to describe the genotype-environmental interactions of a set of genotypes. The first (Finlay and Wilkinson, 1963; Rowe and Andrew, 1964; Eberhart and Russell, 1966; Breese, 1969) is a purely statistical approach, whereas the second (Perkins and Jinks, 1968 a,b; Baker, 1969) and a third derived from it (Freeman and Perkins, 1971) relate the components in the regression analysis to the basic biometrical-genetical model given by Perkins and Jinks (1968 a,b). The definitions of the d_i and gij parameters in this model (No. 1) have been modified, as suggested by Connolly (1968) to allow for heterozygosity in the genotypes (Breese, 1969). Different models used to analysis the data for genotype-environment interaction are as follows.

1. <u>Basic biometrical-genetical model</u>

$$Yij = \mu + di + \varepsilon j + gij \qquad \text{Model 1}$$

Where:

Yij = mean phenotype of the ith genotype in the jth environment.

μ = grand mean over all genotypes and all environments.

di = genetic contribution of the ith genotype.

εj = additive environmental component of the jth environment.

gij = genotype-environmental interaction of the ith genotype in the jth environment.

2. <u>Regression approach 1</u>

$$Yij = xi + \beta i\, \varepsilon j + \delta ij \qquad \text{Model 2}$$

where:

xi = mean expression (i.e. mean overall environments of the ith genotype.

βi = regression coefficient of the ith genotype for the regression of Yij on εj.

δij = deviation, in the jth environment, of the ith genotype from its linear regression on to εj.

3. <u>Regression approach 2.</u>

$$Yij = \mu + di + \varepsilon j + \beta di\, \varepsilon j + \delta ij \qquad \text{Model 3}$$
$$= \mu + di + \varepsilon j\,(1 + \beta di) + \delta ij$$

Where:

di = regression coefficient of the ith genotype for the regression of gij on to εj.

4. <u>Regression approach 3</u>

$$Yij = \mu + di + \bar{\beta} zj + \bar{\delta} j + \beta dizj + \delta dij \qquad \text{Model 4}$$

$$Yij = \mu + di + \beta izj + \delta ij \qquad \text{Model 5}$$

where:

βi = regression coefficient of the ith genotype for the regression of Yij on to zj.

$\bar{\beta}$ = combined regression coefficient (equal to the mean of all βi).

βdi = difference between the regression coefficient of the ith genotype and the combined regression coefficient (i.e. $\beta i - \bar{\beta}$). It is the coefficient for the regression of gij on to zj.

δij = deviation, in the jth environment, of the ith genotype from its linear regression on to zj.

$\bar{\delta} j$ = deviation of the mean of all genotypes in the jth environment from the combined regression line (i.e. $\epsilon j - \bar{\beta} zj$).

δdij = the deviation of the ith genotype from its linear regression on zj in the jth environment minus j (i.e. $\delta ij - \bar{\delta} j$).

In approach 1 (model 2) phenotype (Yij) is regressed on the additive environmental component (ϵj) to give two measures of sensitivity to change in environment. These are the regression coefficient, βi, and the deviations from linear regression mean square, $(\sum_j \delta^2_{ij})/(S-2)$. Equivalent

sensitivity measures, βdi and $(\sum_j \delta^2 ij)/(S-2)$, are obtained in approach 2 (model 3) by the regression of the genotype-environmental component (gij) on the additive environmental component (εj). These two regression approaches are directly related such that xi, βi, and δij are equal to $(\mu + di)$, $(1 + \beta di)$ and δij, respectively. The relation between βi and βdi occurs because in approach 1 the additive environmental component (εj) as well as the genotype-environmental component (gij) is regressed on the εj values and this regression of εj on to itself has a slope of unity. Thus, when approach 1 is followed the regression sum of squares contains additive environmental as well as interaction variation and is equal to $(1 + \beta di)^2 \sum_j (\varepsilon j)^2$ where that following approach 2 is $(\beta di)^2 \sum_j (\varepsilon j)^2$ (Parkins and Jinks, 1968 a,b). The appropriate partition of the total degrees of freedom available from t genomes and s environments is given for each approach as follows.

1. <u>Regression approach 1</u>

	Item	d.f.
	1. Between genotypes (G)	t - 1
	Within genotypes (WG)	t(S-1)
WG	2. Joint regression	1
WG	3. Heterogeneity of regressions	t - 1
WG	4. Deviation from regression	t (S-2)
	Total	ts- 1

II. Regression approach 2

		Item	d.f.
	1.	Between genotypes (G)	t - 1
	2.	Between environments (E)	S - 1
		Genotypes xenvironments (GxE)	(t-1)(S-1)
GxE	3.	Heterogeneity of regressions	t - 1
	4.	Deviations from regression	(t-1)(S-2)
		Total	ts - 1

III. Regression approach 3

		Item	d.f.
	1.	Between genotypes (G)	t - 1
		Between environments (E)	S - 1
E	2.	Combined regression	1
	3.	Environmental residual	S - 2
		Genotypes X environments (G x E)	(t-1)(S-1)
GxE	4.	Heterogeneity of regressions	t - 1
	5.	G x E residual	(t-1) (S-2)
		Total	ts - 1

Because of the relation between the individual regression sums of squares and the equality of the deviations from regression sums of squares, the heterogeneity of regressions

and the deviations from regression items of approaches 1 and 2 are equal.

The estimate of the environmental component used in approaches 1 and 2 has generally been the mean of all genotypes in each environment, calculated from the actual data analysed for its interaction variation. In these cases the environmental values used on the X axis in the regression analysis have not been independent of the phenotypic variable regressed on them. The only exception to this procedure is the regression of progeny phenotypes on additive environmental components estimated from parental phenotypes. Examples where the performance of F_1, F_2 or back-cross individuals has regressed on parental performance may be found in Bucio Alanis and Hill (1966), Perkins and Jinks (1968 a,b), Breese (1969), Bucio Alanis, Perkins and Jinks (1969), Perkins (1970), Jinks and Perkins (1970) and Westerman (1971 a,b).

Considered individually both approaches described in the preceding paragraphs appear to be statistically valid. However, when, as has been the usual procedure, non-independent estimates of ε_j are used, the joint regression sum of squares with one degree of freedom in approach 1 is equal to the environments sum of squares with (S-1) degrees of freedom in approach 2. This ambiguity in assignation of degrees of freedom, noted by Perkins and Jinks (1968 a,b), is considered in detail by Freeman and Perkins (1971) in their examination

of the use of the statistical theory of regression to describe environmental and genotype-environmental variations. They conclude that it is statistically invalid to use non-independent environmental values. This criticism applies, with the exception noted earlier, to all previous work in which approach 1 or approach 2 was followed.

In addition, Freeman and Perkins (1971) criticise the partitioning of the genotype X environment sum of squares into parts attributable to individual genotypes. This partitioning is implicit in any examination of the individual regression lines with approach 2 and, although possible arithmetically, is not valid statistically as too few degrees of freedom are available. The sensitivities of individual genotypes can only be compared by partitioning the total within genotypes sum of squares, which contain both the between environments and the genotype X environment components (Freeman and Perkins, 1971).

To correct the statistical shortcomings of the previous approaches Freeman and Perkins (1971) developed approach 3 in which phenotype (Y_{ij}) is regressed on to independent environmental values (Z_j's). They suggest that the Z_j values be obtained by replication of the genotypes being investigated or by use of control genotypes such as the inbred parents used by Bucio Alanis, Perkins and Jinks (1969).

Perkins and Jinks (1968 a,b), Bucio Alanis *et al.* (1969), Paroda and Hayes (1971), Joarder and Eunus (1978), Joarder *et al.* (1979), and Bains (1976) observed that both linear (βi) and non-linear ($\bar{S}d^2$) components are subjected to genetical control and are at least in part subject to different genetic systems. Our knowledge of the inheritance of this component is as yet limited to investigations with *Nicotiana rustica* reported by Bucio Alanis *et al.* (1969) and to a limited extent in wheat by Bains (1976). These authors showed that it was possible to accurately predict the linear function (βi) of advanced generations of a cross between pairs of pure breeding lines from those observed in the parental and F generations. These they observed by partitioning the genotype-environment interactions into those involving additive effects of the genes and those involving dominant effects.

In spite of the presence of genotype-environment interaction, a breeder is trying to produce a variety with good general adaptations to the whole range of environmental and agronomic conditions of importance and to breed varieties adapted to specific environments within which a selection programme is operating. Genotype-environment interaction is now recognised as an important source of phenotypic variation. As it is under the control of gene, the breeders are able to select suitable genotypes in advanced generations by growing them under different environmental conditions. Knowledge about

the type of genotype-environment interactions involved in populations help the breeder to breed and to select better varieties.

REVIEW OF LITERATURE

Dealing with the problem of genotype-environment interactions to various crop plants a large number of papers have been published. But there are limited number of works dealing with the problems of genotype-environmental interactions shown by coleoptile length in wheat. Some of these available works are reviewed below:

Allan *et al.* (1962) studied fourteen selections of standard height, 25 semidwarf selections of the common type and 16 semidwarf club selections were grown at 50 and 90°F. in the absence of light. The high temperature significantly reduced the coleoptile lengths of wheat selections in all groups as compared with the measurements taken at 50°F. Selection within the standard height and club-type semidwarf groups differed significantly in their sensitivity to high temperature. Amongst the standard height selections, spinkcota, which emerges rapidly, showed least reduction in coleoptile length; Brevor, which emerges slowly, showed the greatest reduction. The semidwarf clubs showed the greatest variability in coleoptile reduction.

Chowdhury and Allan (1963) calculated the heritability values for coleoptile length and seedling height for four winter wheat crosses involving two semidwarf selections and two standard height varieties. Coleoptile length in Royal x SD14 and Nigger x SD50-3-3 had high heritability values and

selection could be practised effectively in the F_2. Effective selection for seedling height was shown to be possible only for Royal x SD14. Results indicated that both major and minor modifying genes controlled the inheritance of these two characters. Positive phenotypic correlations were found between coleoptile length and seedling height for all the crosses; these characters exhibited only a low degree of association with plant height except in the case of Royal x SD14.

Sunderman (1963) found significant differences in percentage emergence and coleoptile length among nine varieties included in field and laboratory tests under different conditions of temperature, depth of sowing. Delmar, while only ranking seventh in height, had the highest percentage emergence and the longest coleoptiles. Variety x depth of planting interaction was highly significant for coleoptile length but not for emergence. Plant height was positively correlated with coleoptile length in three out of five test and with emergence in one out of two tests. Coleoptile length in the laboratory showed highly significant positive correlation with the average coleoptile length and emergence percentage in the field: the highest correlation between coleoptile lengths and emergence percentages in the field tests was obtained at a four inch depth of planting. Thus lines showing better emergence may be derived by the selection

of plants manifesting long coleoptiles either in laboratory test or when planted at a depth of four inches in the field.

Hunt and Miller (1964) reported that seed size, coleoptile length, emergence, and seedling height varied widely in intermediate wheat grass. High positive correlation were found among all characters. Wide variation in all characters was found among the limited number of selections studied. Some evidence of environmental influence on seed size which does not influence coleoptile length was presented. The analysis of a diallel cross indicated a strong maternal influence on coleoptile length.

Burleigh _et al._ (1964) studied the influence of temperature and depth of planting on coleoptile elongation and seedling emergence was used in four normal height and four semidwarf selections. The normal height selection had the greatest coleoptile length and emergence-rate index at 50°F. but not at 90°F. Significant variety x depth of planting interactions occurred at 50°F. but not at 90°F.

Burleigh _et al._ (1964) reported that the temperatures of 80 to 90°F. did not cause comparable reduction in growth of the coleoptile within the eight varieties and selections studied. Red Russian and the semidwarf selections 14 x 53-101 and Norin 10-Brevor 14 were more tolerant of high temperatures than the other varieties and selections and should be of use in breeding

short-strawed winter wheats with coleoptiles tolerant of high temperatures.

Parodi *et al.* (1970) reported F_1 generation of a diallel cross involving the soft red winter wheats Vermillion, Seneca, Knox 62, Benhur, Arthur and Purdue 5215 showed heterosis and heterobeltiosis for coleoptile length. Since the F_2 progenies essentially equalled the midparental values, the F_1 superiority is probably partly due to the larger size of the hand crossed seed. Coleoptile elongation appeared to be controlled largely by additive gene action and heritability was high. In the parents a significant influence of seed size on coleoptile elongation and seedling fresh weight was established.

Roy *et al.* (1970) reported forty varieties differing in height, ranging from varieties carrying three genes for dwarfness to tall varieties, were screened for the response of their coleoptile growth to temperature. A marked positive association of coleoptile length with plant height was observed. Tall varieties developed longer coleoptiles than semidwarf varieties at both 20 and 25°C though growth was less at 25°C. Substantial differences in length of the coleoptile were noted at intravarietal and intervarietal levels for all four height categories considered.

Bains *et al.* (1973) reported that the six generation of two crosses were evaluated for coleoptile length and width.

Overdominance was demonstrated for both traits except in one cross where complete dominance operated. The unfixable component of genetic covariance and the dominance genetic correction between traits were also important. "The partitioning analysis of the generation means indicated the prevalance of dominance gene effects in both crosses for the two traits, except in one cross where a preponderance of additive gene effects was observed for coleoptile length. In the cross Agra Local x Sonora 64-KI. Rend., epistasis was of the additive x additive and dominance x dominance type for both traits; however, in the cross E6402 x HD1949, it was due to additive x additive genic interaction for coleoptile length and to dominance x dominance interaction for coleoptile width. The significant dominance x dominance genic interaction had no reinforcing effect toward genic dominance, indicating the presence of duplicate epistasis in the inheritance of these characters."

Porceddu _et al_. (1974) reported highly significant variation occured in the coleoptile length of 37 _Triticum durum_ lines (including 15F_1 hybrids and some F_2 plants) when seed was germinated at 10, 15, 20 and 25°C. F_1 hybrids had significantly higher values than the mid-parental value at each temperature. Data suggested coleoptile length is governed by polygenic inheritance with an absence of major gene effects. A large proportion of the genetic variability was ascribed to

additive gene effects and a smaller proportion to dominance effects.

Bhatt and Qualset (1975) studied eighteen spring and semiwinter wheat genotypes. The effect of temperature on coleoptile length was found to be suitable for choosing genotypes and management practices to minimize adverse genotype x environmental interactions during the establishment of stands. For each genotype data are tabulated on origin, height and coleoptile length at three establishment temperatures.

Scarascia *et al.* (1975) studies with 1600 *Triticum durum* lines from 18 Mediterranean countries, grown mainly at 15 or 25°C, it is concluded that (1) appreciable variation for coleoptile length exists with *T. durum*, (2) different temperatures seem to induce variation in coleoptile length; (3) different lines have different over-all responses to temperature; (4) culm length and coleoptile length are independent traits; (5) factors involved in coleoptile growth, including length, time of emergence, and temperature requirement, may have different genetic bases; (6) lines carrying Norin [Agriculture and Forestry] and Brevor dwarfing genes fall into the group of lines having low stability at different temperatures; and (7) inheritance of coleoptile length appears to be under polygenic control, with absence of major gene effects, while much of the genetic variability appears to result from additive gene effects.

Agrawal et al. (1976) studied the range, mean, phenotypic and genotypic coefficients of variation, genetic advance and inter-relationship among coleoptile length, seedling height, culm length and grain weight were studied in 100 diverse spring wheat varieties. The varieties differed significantly for the characters studied. The 4 traits were positively associated with each other. Coleoptile length and seedling height influenced culm length. In a few varieties the traits were independent.

Fick and Qualset (1976) studied in a diallel analysis of four dwarf varieties and two varieties of standard height, seedling emergence was closely correlated with coleoptile length and plant height in the parents, F_2 and F_3. Genetic mechanisms that governed plant height also influenced coleoptile length, but the relative effects of genes showing dominant or epistatic effects appeared to be different. Mean F_2 coleoptile length were consistently closer to the low parent value than were corresponding mean F_2 plant heights. A slight curvilinear relationship was found between coleoptile length and plant height of F_3 lines.

Whan (1976) reported that the emergence of ten semidwarf and standard varities from four sowing depths was measured under different soil conditions in two years. A significant variety x depth interaction was observed. The emergence results obtained were directly related to the coleoptile lengths of

the varieties. The semidwarf wheats had shorter coleoptiles than the standard varieties, so the depth at which their emergence was reduced was shallower than for the standard varieties. A close correlation between mature plant height and coleoptile length within the semidwarf varieties studied was observed.

Whan (1976) reported that the coleoptile length was positively correlated (r = 0.76) with culm length at maturity in the 56 semidwarf varieties studied but not (r = 0.07) in the 40 standard varieties; when Ghurka derivatives (long coleoptile) were excluded from the standard varieties, the latter correlation was r = 0.56. Fiftyfour of the semidwarf varieties had shorter coleoptiles than the standard varieties, although some of them were as tall at maturity as the standard varieties. Most of the standard varieties from Victoria had very long coleoptiles.

Virk _et al._ (1977) studied parental generations, F_1, F_2, BC_1 and BC_2 of tall x tall, semidwarf x semidwarf and tall x semidwarf crosses involving four varieties, analysis of means and variances indicated that considerable fixable genetic variation is available for coleoptile length and width crosses within tall and semidwarf groups. A simple additive-dominance model was inadequate in the analysis of means, but failure as a result of maternal effects or nonallelic interactions could not be identified as reciprocal crosses were not available.

Gill *et al.* (1981) reported combining ability for coleoptile length in diallel crosses involving seven diverse wheat cultivars in generations F_2 to F_6. The general combining ability variances were significant in all the generations and their magnitude consistently increased over that of specific combining ability variances with the advancement of generations establishing clear predominance of additive genetic system for this attribute. The ratio of GCA:SCA variances was also quite high in all the filial generations substantiating the operation of additive genetic system for coleoptile length. However, the specific combining ability variances were observed to be significant in the F_2 and F_3 generations only and not in the latter generations. The general combining ability estimates were quite consistent over the generations and depicted repeatability over all the measured generations. In view of repeatability of GCA estimates over the generations, the possibility of early detection of prepotent parents for greater coleoptile length and their simultaneous exploitation has been discussed. The two cross combinations namely Sonalika x Sharbati Sonora and C273xK68 giving positively significant specific effects in an advanced generation like F_6 offer the best possibilities of exploitation for the development of desirable lines.

Sharma *et al.* (1982) described that the interrelationship between grain yield, culm length and their component traits were studied in F_1 and F_2 progenies in spring wheat. Culm length

was positively correlated with coleoptile length, seedling height and peduncle length. Among themselves too these component traits showed positive and significant relatiionship. Grain yield exhibited positive association with 100 grain weight, coleoptile length, seedling height, peduncle length and culm length. 100-grain weight also showed positive relationship with these traits. Dwarf lines having long coleoptile and peduncle were isolated.

MATERIALS AND METHODS

A. MATERIALS:

The present investigation comprised eight separate experiments. The materials used in each of the experiments are described below:

Experiments 1, 2 and 3:

The twelve genotypes of wheat (*Triticum aestivum* L. em Thell) listed below were selected from the germplasm collection of the Plant Breeding Laboratory, Department of Botany, Rajshahi University as the base material of the present study. The comparative coleoptile length and linear components (b_i) of the twelve genotypes were as follows:

	Genotypes	Comparative coleoptile length	Linear components (b_i)
1.	Sonora - 64	Low	low
2.	Mexipak - 65	Low	high
3.	Innia - 66	medium	high
4.	Norteno - 67	medium	high
5.	Sonalika	low	low
6.	Tanori - 71	low	low
7.	Jupatica - 70	medium	high
8.	Noori	low	low
9.	Penkty	medium	high

	Genotypes	Comparative coleoptile length	Linear components (b_i)
10.	Janak	medium	low
11.	Dirk	high	low
12.	Kazoli	high	high

Experiment 4:

The materials used in this experiment consisted of two wheat genotypes together with their F_1 and 60 inbred lines derived from seven and eight successive generations of selfing from single, randomly chosen, F_2 plants of the cross made between the two parental genotypes.

	Genotypes	Comparative coleoptile length	Linear components (b_i)
1.	Mexipak-65	low	high
2.	Janak	high	low

At the beginning of the study, the plant Breeding Laboratory, Department of Botany, Rajshahi University was kind enough to supply the seeds of parental genotypes, Mexipak - 65 and Janak together with the selected seeds of 60 inbred lines of F_6 generations.

Experiment 5:

The material consists of 10 inbred lines randomly chosen from the 60 inbred lines used in experiment 4.

Experiment 6:

The ten wheat genotypes listed below were selected on the basis of their differences in coleoptile length.

	Genotypes	Comparative Coleoptile length	Linear components (b_i)
1.	Sonora - 64	low	low
2.	Mexipak - 65	low	high
3.	Innia - 66	medium	high
4.	Norteno - 67	medium	high
5.	Sonalika	low	low
6.	Tanori - 71	low	low
7.	Jupatica - 70	medium	high
8.	Penkty	medium	high
9.	Dirk	high	low
10.	Kazoli	high	high

They were crossed in a diallel fashion in all possible combinations including reciprocal producing the 90F_1 hybrids. Therefore, the above mentioned 10 genotypes and the 90 F_1S constituted the materials of this experiment.

Experiment 7:

Six genotypes of wheat selected for the present study are as follows:

	Genotypes	Comparative coleoptile length
1.	Sonora - 64	low
2.	Mexipak - 65	low
3.	Sonalika	low
4.	Penkty	low
5.	Dirk	high
6.	Kazoli	high

Eight single crosses were made without reciprocal between the selected parents and F_1, F_2, F_3, F_4, B_1 and B_2 generations were obtained. Parents and their segregating and non-segregating generations constituted the materials for this experiment. The single eight crosses were as follows:

Cross No.	Cross combination
Cross 1	Kazoli x Sonora- 64
Cross 2	Dirk x Sonora- 64
Cross 3	Kazoli x Mexipak- 65
Cross 4	Dirk x Mexipak - 65
Cross 5	Kazoli x Penkty
Cross 6	Dirk x Penkty
Cross 7	Kazoli x Sonalika
Cross 8	Dirk x Sonalika

Seeds used in this experiments were received from the seed stock maintained at the Department of Botany, University of Rajshahi.

Experiment 8:

The six wheat (*Triticum aestivum* L. em Thell.) genotypes listed below were selected from the germplasm collection of the Department of Botany, Rajshahi University on the basis of their known performance of coleoptile length and the linear and non-linear components of their genotype-environment interactions.

Genotypes	Comparative Coleoptile length	Linear components(b_i)	Non-Linear components $\bar{S}^2d$
1. Sonora- 64	medium	low	low
2. Sonalika	medium	low	low
3. Janak	medium	low	high
4. Jupatica-70	low	high	low
5. Penkty	high	high	high
6. Mexipak- 65	low	high	low

On the basis of b_i components six crosses were made. They are as follows:

Cross No.	Cross combination		Properties of b_i
Cross 1	Sonora-64	x Penkty	high x low
Cross 2	Sonalika	x Mexipak-65	high x low
Cross 3	Sonora-64	x Janak	low x low
Cross 4	Sonalika	x Janak	low x low
Cross 5	Jupatica-70	x Penkty	high x high
Cross 6	Mexipak-65	x Penkty	high x high

Therefore, two of the crosses (cross 1 and cross 2) were between pairs of parents, one of which has a low sensitivity (low b_i) and the other a high (high b_i value) sensitivity to the environments, i.e. 'low x high'; similarly, two of the crosses (cross 3 and cross 4) were between pairs of parents with low sensitivities (low b_i values) to the environment, i.e. 'low x low'; and also two of the crosses (cross 5 and cross 6) were between pairs of parents with high sensitivities to the environment, i.e. 'high x high'. For each of the six crosses F_2, F_3 and F_4 generations were obtained.

For F_3 generation, $30F_3$ progenies each derived from a single randomly chosen $30F_2$ plants for each of the six crosses. For F_4 generation, 30 families of F_4 generation of each cross were obtained by bulking the seeds from individuals within each of the corresponding $30F_3$ families. (Approximately 75%

seeds of a selected F_2 plants were used for study as F_3 generation and the rest of the seeds were raised in the field to get F_4 seeds).

B. METHODS:

The methods followed to conduct experiments and analysis of data were subdivided into the following heads:

(a) Collection of Experimental Seeds

(b) Environments

(c) Experimental Procedure

(d) Collection of Data

(e) Techniques of Analysis of Data

(a) Collection of the Experimental Seeds

Base material for all the experiments were collected from raising respective genotypes at the Botanical Research Garden of Rajshahi University. In all the eight experiments fresh seeds were used every year by raising the genotypes during winters of 1978 to 1982. The experimental fields were prepared as homogeneously as possible through repeated ploughing. During the preparation of the field oil cake and cowdung were added at the rate of 820 and 1980 kg/hectare respectively as a source of organic manures. Urea, triple-super-phosphate (T.S.P.) and muriate of potash were added at the rate of 80, 60 and 40 kg/hectare respectively.

Seeds of each genotype were made a continuous line sowing rather thind to an optimum level. The space between the lines

within a block was 30 cm. Seeds were harvested when properly matured, usually in the 3rd-4th week of March in each year.

Soil moisture was kept optimum through irrigation whenever it was necessary. Irrigation was done on the day following sowing of seeds for uniform germination of the seeds. Three more irrigations were given; first at the time of tillering, second after 20 days of the first irrigation and third at the time of grain filling stages. The usual weeding was done whenever necessary.

Experiment 1, 2 and 3:

Twelve genotypes were the materials of these experiments. The twelve genotypes were sown in the field on the 15th November of 1978, 1979, 1980, 1981 and 1982 in a randomized block design. There were four replications in each year and the twelve genotypes were randomly assigned within a replication. For each genotype per replication there was a block of 3m x 4m size. The space between blocks and all around the field was 1.5m and 2m respectively.

Experiment 4 and 5:

Seeds of two genotypes and their 60 inbred lines of F_6 and F_7 generations were sown in the field on the 15th November

of 1980 and 1981 respectively. There were four replications in each year and the two genotypes and their 60 inbred lines were randomly assigned within a replication. For each genotype per replication there were three single row plots of 3m size which were arranged randomly. The space between replication and all around the field was 1.5m and 2m respectively. The space between the plots was 30 cm.

Parents, F_6 and F_7 plants were selfed to get fresh parental, F_7 and F_8 seeds respectively. Seeds collected in this way were used in the experiments of 1981 and 1982.

Fresh crosses were made between parental genotypes to get F_1 seeds for the experiments. Crosses were made in separate crossing blocks.

Experiment 6:

Ten wheat genotypes were sown in the field on 15th November, 1981 in a randomized block design. There were four replications and the ten genotypes were randomly assigned within a replication. For each genotype per replication there was a block of 3m x 4m size. The space between blocks was 1.5m and space around the field was 2m.

For F_1 seeds, ten genotypes were crossed in a diallel fashion in all possible combination including reciprocal producing 90F_1 seeds. Seeds collected in this way were used in this experiment.

Experiment 7:

Seeds of six genotypes, F_1, F_2 and $15F_3$ families (for F_3 generation, $15F_3$ progenies each derived from a single randomly chosen $15F_2$ plants for each of the eight crosses) of eight crosses were sown in the field on the 15th November, 1981. Parental genotype, F_1, F_2 and $15F_3$ families were selfed to get fresh parental, F_2, F_3 and F_4 seeds. F_4 seeds were collected from randomly selected $15F_3$ plants from each of the $15F_3$ generations of each cross.

Fresh F_1 seeds were obtained by crossing appropriate parental genotypes, and the backcross seeds of each cross were obtained by backcrossing F_1 to the appropriate P_1 and P_2. Seeds collected in this way were used in this experiment.

Experiment 8:

Seeds of six parental genotypes, F_2 and F_3 generations of six crosses were sown in the field on the 15th November, of 1979, 1980, and 1981. There were three replications and the six genotypes, F_2 and F_3 were randomly assigned within a replication. For each genotype per replication there were three 3m. single row plots. The space between plots, replication and all around the field was 30cm., 1.5m. and 2m. respectively.

Fresh F_1 seeds were obtained by crossing appropriate genotypes, and seeds collected in this way were used in the experiments in 1980, 1981 and 1982.

(b) Environments:

Environments used in the different experiments were effects of different temperature and different germinating medium on coleoptile length. The different environments used in the different experiments were as follows:

Experiment 1:

The environments used in the study were effects of different temperature on coleoptile length.

The germinating seeds were raised in a temperature control incubator till the first leaf appeared, at temperatures of 20°, 25°, 30°, 35° and $40^{\circ}C$ in five separate runs. Therefore, these five effects of different temperature on coleoptile length will be treated as environment in this experiment.

Experiment 2:

In this experiment the environments used were eight different nutritional germinating medium on coleoptile length. The seedlings were raised at a constant temperature of $28^{\circ}C$. The nutritional mediums were as follows:

1. $Nacl_2$ - 0.2%
2. $Nacl_2$ - 0.5%
3. $Nacl_2$ - 0.7%

4. $NaCl_2$ - 1.0%
5. $Na(OH)_2$ - High PH
6. $Ca(OH)_2$ - High PH
7. Hcl - Low PH
8. Control - Distilled water

Experiment 3, 4 and 5:

Sixteen different germinating mediums were used as the environments of these experiments. They were produced in combination of presence or absence of Nitrogen (N), Phosphorus (P), Potassium (K), and Calcium (Ca); the combination being N, P, K, Ca, NP, NK, NCa, PK, PCa, KCa, NPK, NPCa, NKCa, PKCa, NPKCa and control (distilled water). The source of N,P,K and Ca were:

(1) N - Urea (0.2% solution were used)
(2) P - Triple Super Phosphate (0.2% solution were used)
(3) K - Muriate of Potash (0.2% solution were used)
(4) Ca - Calcium hydroxide (2.0% solution were used)

Experiment 6 and 7:

The environments used for these experiments were the same as those described in experiment 1.

Experiment 8:

The germinating seed containing high and low PH of germinating medium were raised in a temperature control incubator

till the emergence of first leaf. The temperatures were 28°, 20°, 25°, 30°, and 35°C. Therefore five different effects of temperature and two different germinating mediums of high and low PH on coleoptile length were treated as environment in this experiment. They were as follows:

Temperature	Germinating medium
28°C	Distilled water
20°C	High PH - $Ca(OH)_2$
	Low PH - Hcl
25°C	High PH - $Ca(OH)_2$
	Low PH - Hcl
30°C	High PH - $Ca(OH)_2$
	Low PH - Hcl
35°C	High PH - $Ca(OH)_2$
	Low PH - Hcl

High and low PH was made by adding calcium hydroxide $Ca(OH)_2$ and hydrocloric acid (Hcl) respectively.

(c) Experimental Procedure

Healthy seeds of uniform size were raised on moist filter paper in petridishes. One petridish (100mm.), accommodating 15 seeds, was used for each genotype. The seeds were first placed on the petridishes, properly labelled, were shocked with

distilled water for about 15 to 20 minutes and then the petridishes containing germinating seeds were kept on the shelves in a temperature control incubator to study effects of temperature on coleoptile length. The incubator had four shelves and the shelves were treated as replication. The petridishes containing germinating seeds on a shelf were rearranged every morning within a shelf to minimize position effects.

The petridishes containing the germinating seeds were kept in an incubator. The petridishes were removed from the incubator when the primary leaf had ruptured the coleoptile. The seedlings were removed from the petridishes and coleoptile length recorded to the nearest millimeter.

Experiment 1:

Seeds of twelve genotypes were raised together in a temperature control incubator during 1st May to 10th June, 1978, 1979, 1980, 1981 and 1982. Environments used in the study were five effects of different temperature on coleoptile length. There were altogether 12 petridishes per replication. Therefore, 48 petridishes were used for the four replications in each of the five effects of temperature on coleoptile length.

seeds were kept in a temperature control incubator, throughout the experiment, at a fixed temperature of 28°C.

The whole experiment was replicated four times. The following are the dates when four replication were given in each year.

Date in each of 1978, 1979 and 1980	Genotypes raised/ replication	Fixed temperature
20th June (Replication I)	12 genotypes	28°C
30th June (" II)	Do	Do
10th July (" III)	Do	Do
20th July (" IV)	Do	Do

Experiment 3:

Seeds of twelve genetypes were raised together in a temperature control incubator during 30th July to 29th August, 1978, 1979, 1980 and 1981. Environments used were sixteen different combinations of NPKCa germinating medium as mentioned under the head Environment. There were altogether 192 petridishes per replication. 10cc of each of the sixteen different NPKCa combination were supplied to each of the twelve genotypes and then all the petridishes containing germinating seeds were kept in a incubator throughout the experiment at a fixed temperature of 28°C.

The whole experiment was replicated four times. The following are the dates when four replications were given in each year.

Date in each of 1978,1979,1980 & 1982	Genotypes raised/ replication	Fixed temperature
30th July (Replication I)	12 genotypes	28°C
9th August (" II)	Do	Do
19th August (" III)	Do	Do
29th August (" IV)	Do	Do

Experiment 4 and 5:

The 60 imbred lines together with the two parental genotypes and their F_1 were raised in a temperature control incubator from 1st September, 1981 to 1982. Environments used were sixteen different combination of NPKCa germinating medium as mentioned under the head Environment. There were altogether 63 petridishes per replication. Therefore, 252 petridishes were used for the four replications in each of the sixteen different combinations of NPKCa germinating medium.

10 cc. of each of the sixteen NPKCa germinating medium were supplied to each of the genotypes and then all the petridishes containing the germinating seeds were kept in an incubator throughout the experiment, at a fixed temperature of

$28^{o}C$. The whole experiment was set up sixteen times. The following are the dates when sixteen different environmental medium were given:

Date	Genotypes raised in four replication	Environment
1st September, 1981	P_1, P_2, F_1 & their 60 inbred line	N
11th September, 1981	Do	P
21st September, 1981	Do	K
1st October, 1981	Do	Ca
11th October, 1981	Do	NP
21st October, 1981	Do	NK
31st October, 1981	Do	NCa
10th November, 1981	Do	PK
20th November, 1981	Do	PCa
30th November, 1981	Do	KCa
10th December, 1981	Do	NPK
20th December, 1981	Do	NPCa
30th December, 1981	Do	NKCa
9th January, 1982	Do	PKCa
19th January, 1982	Do	NPKCa
29th January, 1982	Do	Control

Experiment 6:

Seeds of ten wheat genotypes and their 90F_1S were raised together in a temperature control incubator from the 1st May,

1982. Environment used in this investigation were five different temperature as mentioned under the head Environment. There were altogether 100 petridishes per replication. Therefore, 400 petridishes were required for four replications in each of the five different temperature.

The petridishes containing germinating seeds were shocked with distilled water and then kept in temperature control incubator throughout the experiment, at temperatures of 20°, 25°, 30°, 35° and 40°C in five separate runs. The whole experiment was set up five times. The following are the date when five different temperatures were given.

Date	Genotypes raised in four replication	Environment
1st May, 1982	Parents and their 90F_1S	20°C
11th May, 1982	Do	25°C
21st May, 1982	Do	30°C
31st May, 1982	Do	35°C
10th June, 1982	Do	40°C

Experiment 7:

Seeds of six genotypes and their F_1, F_2, F_3, F_4, B_1 and B_2 generation of eight crosses were raised together in a temperature control incubator on 20th June, 1982. The number of petridishes of different generations of a cross were one

for each of P_1, P_2, F_1, B_1 and B_2 generations; five for F_2 generations and one for each of the 15F_3 families and one for each of the 225F_4 families. There were altogether 250 petridishes per replication. Therefore, 1000 petridishes were used for four replications. 10cc. of distilled water was supplied to each of the genotypes and then all the petridishes containing the germinating seeds were kept in a incubator throughout the experiment at temperature of 20°, 25°, 30°, 35° and 40°C in five separate runs.

Experiment 8:

Seeds of six genotypes and their six crosses of F_2, F_3 and F_4 generations were raised together in a temperature control incubator during 1st October, 1980, 1981 and 1982. The environments used in this investigation were five different temperatures. In each temperature the PH of the germinating medium was high and low as mentioned under the head Environment. There were altogether 24 petridishes per replication. Therefore 48 petridishes were required for two replication in each of the five effects of different temperature and different germinating medium.

10 cc. of each of the different germinating medium of high and low PH of $Ca(OH)_2$ and Hcl were supplied to each of the genotypes and then all the petridishes containing the germinating seeds were kept in an incubator throughout the

experiment at required temperature in nine separate runs. The following are the date when seeds were germinated under the given environments in each year.

Date in each of 1980, 1981 and 1982	Generation raised in two replication		Environments
1st October, 1980	Parents, F_2, F_3 & F_4	28°C	Distilled water
11th October, 1980	Do	20°C	High PH-$Ca(OH)_3$
21st October, 1980	Do		Low PH-Hcl
31st October, 1980	Do	25°C	High PH-$Ca(OH)_3$
10th November, 1980	Do		Low PH-Hcl
20th November, 1980	Do	30°C	High PH-$Ca(OH)_3$
30th November, 1980	Do		Low PH-Hcl
10th December, 1980	Do	35°C	High PH-$Ca(OH)_3$
20th December, 1980	Do		Low PH-Hcl

(d) Collecting of Data

Data on coleoptile length were recorded on an individual plant basis. The coleoptile length of the ten germinating seedling per petridishes were measured to the nearest milli-meter when the first (primary) leaf was found to develop completely. This usually took 5 to 7 days. For all the experiments, data were collected in the same way as described above.

At the beginning of my study, plant Breeding Laboratory, Department of Botany, Rajshahi University was kind enough to supply the data of experiment 1 for the year 1976, 1977 and of experiment 2 for the year 1977.

(e) Techniques of Analysis of Data

Biometrical techniques of analysis developed by Mather (1949), Mather and Jinks (1971, 1977) based on the mathematical model of Fisher *et al.* (1932) and those of Hayman (1958) and Allard (1960) were followed to analyse the recorded data.

Means and Variances:

Means and variances were calculated as follows:

$$\text{Mean } (\bar{X}) = \frac{\Sigma x_i}{n}$$

$$\text{Variance } (\delta^2) = \frac{1}{n-1}\left[\Sigma x_i^2 - \frac{(\Sigma x_i)^2}{n}\right]$$

where, X_i is the value of individual observation and n is the number of total observations. The different sources of variations calculated were genotypic, environmental and their interactions.

The environmental indices (I_j) were obtained by subtracting the overall mean from each of the environmental mean

which was as follows:

$$I_j = \frac{\sum_j Y_{ij}}{t} - \frac{\sum_i \sum_j Y_{ij}}{S} \quad (i = 1, 2 \ldots\ldots t \text{ and } j = 1, 2 \ldots\ldots S)$$

$$= \frac{\text{Total of all varieties at jth location}}{\text{Number of varieties}} - \frac{\text{Grand total}}{\text{Total number of observations}}$$

where, t stands for genotypes and S stands for environments.

Dependent ($\sum j$) and independent (Z_j) environmental values were deferentially Fripp and Caten (1971) and Fripp (1972) as follows:

(a) Dependent $\sum_j$

The performance of each of the 12 genotypes and 60 inbred lines was regressed against the mean of all 12 genotypes and of all 60 lines in each environment, i.e. the material used for the environmental assessment is the same as that to be investigated (experiment 1, 2, 3 and 4).

(b) Independent Z_j using replicate individuals.

Each genotype and each inbred lines in each environment was represented by ten individual seedlings. These were split at random into two groups of five, the interactions of one

group to be investigated and the other group contributing to the environmental assessment (experiment 1, 2, 3 and 4).

(c) Independent $\hat{Z}_j$ using replicate sets of genotype and inbred lines.

The 12 genotypes and 60 inbred lines were divided at random into two sets of 6 and 30, the interactions of one set to be investigated and the other set to assess the environment (experiment 1, 2, 3 and 4).

(d) Independent $\hat{Z}_j$ using parents

The 60 inbred lines were regressed against the average of the two parents, Mexipak- 65 and Janak, in each environment from whose F_2 they were derived by selfing. (Experiment 4).

Variability:

The phenotypic variance was repartitioned into genotypic, environmental and genotype x environment interaction variation from the components analysis of variance assuming a mixed model with a fixed number of genotypes (g) and a random sample of environments (e) with (r) replications. The expection of mean squares are as follows:

Source	M.S.	Expectation of M.S.
Genotype (G)	M_1	$\delta^2_W + r\delta^2_{GE} + re\delta^2_G$
Environment (E)	M_2	$\delta^2_W + rg\delta^2_E$
GxE	M_3	$\delta^2_W + r\delta^2_{GE}$
Error	M_4	δ^2_W

Where δ^2_E, δ^2_G and δ^2_{GE} are environmental, genotypic and GxE variances respectively. The genotypic, environmental and GxE variances (δ^2_G, δ^2_E and δ^2_{GE}) were calculated as follows:

$$\delta^2_G = (M_1 - M_3)/(r x e)$$

$$\delta^2_{ge} = (M_3 - M_4)/r$$

$$\delta^2_e = (M_2 - M_4)/r \times g$$

$$\delta^2_W = M_4$$

Stability parameters:

The two parameters of stability were calculated following Eberhart and Russell's (1966) as follows:

(a) <u>Phenotypic Regression</u> (b_i): Response or coefficient of regression 'b_i' is the regression of the performance of each variety under different environments on the environmental

means over all the genotypes. This was estimated as follows:

$$'b_i' = \sum_j Y_{ij} I_j \;/\; \sum_j I_j^2$$

where, $\sum_j Y_{ij} I_j$ is the sum of products and

$\sum_j I_j^2$ is the sum of squares.

standard errors of $'b_i'$ was calculated as follows:

$$S.E_{(b)} = \sqrt{\frac{\text{M.S due to pooled deviation}}{\sum_j I_j^2}}$$

where, M.S. due to pooled deviation $= \sum_j Y^2_{ij} - (Y^2_{ij}/g)$

Barthett's chi-square (X^2) testing the homogeneity of S_b were determined in the following way:

$$X^2 = \text{loge}^{10} \text{ (df. of individual } S^2\text{) } (n\log\bar{S}^2 - \sum \log S^2)$$

where, S^2 = Variance = S^2_b and $\text{Loge}^{10} = 2.3026$

(b) Stability ($\bar{S}^2d$): (Experiment 8). The stability parameter ($\bar{S}^2d$) was calculated as the mean square deviation from the linear equation (Eberhart and Russell, 1966) which was as follows:

$$\bar{S}^2d = \sum_j d^2_{ij} \;/\; (E-2) - (S^2_e / r)$$

Now the variance due to deviation from regression ($\sum \delta^2 ij$) from a replication being

$$\sum_j \delta^2_{ij} = \left[\sum_j Y^2_{ij} - \frac{Y^2_i}{E} \right] - \frac{(\sum_j Y_{ij} I_j)^2}{\sum_j I_j^2}$$

where, $\sum_j Y_{ij}^2 - \frac{Y_i^2}{E}$ = the variance due to dependant variable and

$(\sum_j Y_{ij} I_j)^2 / (\sum_j I_j^2)$ = the variance due to regression.

E is the number of environments and S^2_e is the estimate of pooled error from analysis of variance and r is the replication.

Correlations:

The relationship between two or more than two variables is called correlation. It was measured in the following way:

Correlation (r) = Cov (x.y) / $(V_x . V_y)^{\frac{1}{2}}$

where Cov (x.y) is the co-variance between X and Y,

V_x is the variance of X and

V_y is the variance of Y.

The calculated correlations were tested with (n-2) degrees of freedom.

Diallel analysis:

Graphical Analysis: Techniques as developed by Jinks and Hayman (1953), Jinks (1954), Hayman (1954b) and Johnson and Aksel (1959) were followed for the graphical evaluation of additive (D), dominance (H) gene action and non-allelic interaction present in the diallel cross system. The following statistics were calculated in terms of genetical and environmental components of variation.

V_{OLO} = (V_P) = Variance of parents = D + E,

V_r = The variance of the rth array = $\frac{1}{4}D - \frac{1}{4}F_r + \frac{1}{4}H_1 + [E + \frac{1}{2}(n-1)] E^1/n$,

W_r = The covariance between parents and their offispring in the rth array = $\frac{1}{2}D - \frac{1}{4}F_r + E/n$,

V_{OLI} = $V_{\bar{r}}$ = The variance of array means = $\frac{1}{4}D - \frac{1}{4}F + \frac{1}{4}H_1 - \frac{1}{4}H_2 + [E + \frac{1}{2}(n-2)E^1] / n^2$

V_{ILI} = Mean of the V_rS = $\frac{1}{4}D - \frac{1}{4}F + \frac{1}{4}H_1 + [(E + 1)/ 2(n-1)E^1] /n$,

W_{OLOI} = Mean of W_rS = $\frac{1}{2}D - \frac{1}{4}F + E/n$ and

$(MLI\text{-}MLO)^2$ = square of difference between progeny means and parental means = $\frac{1}{4} h^2 + (n-1) [(n-1)E + E^1] /n^3$.

The plotting of W_r against V_r provides a detail of dominance relationship of the parents with (V_r, W_r) points distributed along a straight line of unit slope inside the limiting parabola, $W_r^2 = V_r V_p$ drawn. In the absence of non-allelic interaction $W_r - V_r = \frac{1}{4}(D-H_1)$, which is independent of signs of the alleles in the parents. This implies that the difference is constant over arrays, and the regression of W_r on V_r should give a straight line of unit slope. If V_r is zero, W_r becomes $\frac{1}{2}(D-H_1)$ so that the regression line for W_r on V_r will intersect the W_r axis above, at or below the point of origin as dominance is incomplete, complete or greater than D respectively. When H is zero, there is no regression and the array variances and covariances estimate the point $(W_r, V_r) = (\frac{1}{2}D, \frac{1}{4}D)$.

The W'_r/W_r graph (where W'_r = covariance between the offspring of the rth array and the array means) is also used to detect the order of dominance of the parents, it is much less affected by genetic disturbances than the W_r/V_r graph and virtually undisturbed by the level of inbreeding (Hayman, 1958). The W'_r/W_r graph differs from the W_r/V_r in that it is more obviously affected by asymmetry of gene distribution and this is indicated whether the genes are correlated or not (Hayman, 1958). With gene symmetry the regression of W'_r on W_r is a straight line of a slope of

+0.5, when gene asymmetry occurs, parents with common genotypes will full above the line of +0.5, parents with different or relatively rare genotypes will fall below it.

Components of Variation and their Ratios: The genetical analysis of continuous variation depends on two simultaneous calculations, first calculation of different statistics from the observed data, second derivation of different components of variation from the calculated statistics. They are as follows:

D (Additive effect of gene) = $V_{OLO} - E$,

H_1 (Dominance effect of genes) = $V_{OLO} - 4W_{OLOI} + 4V_{ILI} - (3n-2)E/n$,

H_2 (Dominance indicating asymmetry of positive and negative effect of genes) = $4V_{ILI} - 4V_{OLI} - 2E$,

h^2 (dominance effect over all loci) = $4(MLI-MLO)^2 - 4(n-1)E/n^2$,

F (Mean of F_r over arrays) = $2V_{OLO} - 4W_{OLO1} - 2(n-2)E/n$

and E (Environmental variation).

The genetic components of variation provided the following ratios.

(a) $\sqrt{(H_1/D)}$ = measures the average degree of dominance over all loci;

$\sqrt{(H_1/D)}$ = 1, indicates comple dominance,

$\sqrt{(H_1/D)}$ = 0, indicates no dominance,

$\sqrt{(H_1/D)}$ = >0 and <1, indicates partial dominance,

and $\sqrt{(H_1/D)}$ = >1, indicates overdominance.

(b) $H_2/4H_1$ = 0.25 is an estimate of the frequency of negative versus positive alleles at loci exhibiting dominance;

(c) h^2/H_2 = an estimate of the number of groups of genes which control the characters and exhibit dominance to some degree.

(d) $\frac{1}{2}F/\left[D(H_1-H_2)\right]^{\frac{1}{2}}$ = on measure of consistency of h to d over all loci.

The heritability both in broad and narrow sense were calculated using the formula given by Mather and Jinks (1971).

$$\text{Broad sense} = \left[\tfrac{1}{2}D+\tfrac{1}{2}H_1 - \tfrac{1}{4}H_2-\tfrac{1}{2}F\right] / \left[\tfrac{1}{2}D+\tfrac{1}{2}H_1 - \tfrac{1}{4}H_2 - \tfrac{1}{2}F + E\right]$$

$$\text{Narrow sense} = \left[\tfrac{1}{2}D+\tfrac{1}{2}H_1 - \tfrac{1}{2}H_2 - \tfrac{1}{2}F\right] / \left[\tfrac{1}{2}D + \tfrac{1}{2}H_1 - \tfrac{1}{4}H_2 - \tfrac{1}{2}F + E\right]$$

<u>Hayman's Analysis of Variance</u>: The technique of Hayman (1954a) analysis of diallel table was followed to analyse the variance of family mean values of diallel tables in order to show the following relationships of the components of variation:

a = (additive effect) = $D-F+H_1-H_2$

b = (dominance effect) = H_2

b_1 = (over all difference between parent and progenies) = h^2

b_2 = (constant dominance effect) = H_1-H_2

b_3 = (residual effect).

c = average maternal effects

d = reciprocal difference not ascribable to c.

Components of generation mean:

<u>3-Parameter model</u>: The expectation of generation means in terms of m, d and h of segregating and non-segregating generations are as follows :

$$\bar{P}_1 = m + d,$$
$$\bar{P}_2 = m - d,$$
$$\bar{F}_1 = m + h,$$
$$\bar{F}_2 = m + \tfrac{1}{2}h,$$
$$\bar{F}_3 = m + \tfrac{1}{4}h,$$
$$\bar{F}_4 = m + 1/_8h$$

$$\bar{B}_1 = m + \tfrac{1}{2}d + \tfrac{1}{2}h,$$
$$\bar{B}_2 = m - \tfrac{1}{2}d + \tfrac{1}{2}h$$

where 'm' measures base population mean, 'd' measures the additive gene effects and 'h' measures the dominance gene effects.

The estimates of m, d and h were done following a weighted least square technique (Fisher, 1946; Mather, 1949: Scorle, 1966; Mather and Jinks, 1971). The detail descriptions of the techniques have been shown by Mather and Jinks (1971). The weights used were the reciprocal of the squared standard errors of respective generations as follows:

$$P_1 = 1/(V\bar{P}_1),\ P_2 = {}^{1/}(V\bar{P}_2),\ F_1 = {}^{1/}(V\bar{F}_1),$$
$$F_2 = {}^{1}/V\bar{F}_2),\ F_3 = {}^{1/}(V\bar{F}_3),\ F_4 = {}^{1/}(V\bar{F}_4),$$
$$B_1 = {}^{1/}(V\bar{B}_1) \text{ and } B_2 = {}^{1/}(V\bar{B}_2).$$

where, $V\bar{P}_1$, $V\bar{P}_2$, $V\bar{F}_1$, $V\bar{F}_2$, $V\bar{F}_3$, $V\bar{F}_4$, $V\bar{B}_1$ & $V\bar{B}_2$ are the standard errors of P_1, P_2, F_1, F_2, F_3, F_4, B_1 and B_2 generations respectively.

The adequacy of the additive dominance models were tested by predicting the eight family means from the estimates of the 3-parameters. The goodness of fit was then tested by squaring the deviations of the observed from

expected values for each of the eight family, multiplying by the corresponding weight and summing the product (over all eight types) of families. The summed value obtained from eight families gave a X^2 for 5 d.f. If X^2 is significant it means that additive dominance model is inadequate and the estimates of the 3-parameter were biased to an unknown extent by effect not attributable to the additive and dominance action of the genes.

<u>6-parameter model</u>: Where 3-parameter model is not suitable to interpret the gene action due to non-allelic gene interaction, the data were analysed following the 6-parameter model of Hyman (1958). The expectation of generation means in terms of 6-parameter model were as follows:

$$\bar{P}_1 = m + d + i,$$
$$\bar{P}_2 = m - d + i,$$
$$\bar{F}_1 = m + h + l,$$
$$F_2 = m + \tfrac{1}{2}h + \tfrac{1}{4}l,$$
$$\bar{F}_3 = m + \tfrac{1}{4}h + {}^{1}/_{16}l,$$
$$\bar{F}_4 = m + {}^{1}/_{8}h + {}^{1}/_{64}l,$$
$$\bar{B}_1 = m + \tfrac{1}{2}d + \tfrac{1}{2}h + \tfrac{1}{4}l + \tfrac{1}{4}j + \tfrac{1}{4}l,$$
$$\bar{B}_2 = m - \tfrac{1}{2}d + \tfrac{1}{2}h + \tfrac{1}{4}i - \tfrac{1}{4}j + \tfrac{1}{4}l$$

where, m = measure the base population mean,

d = measure additive gene effects,

h = measure dominance gene effects,

i = measure additive x additive type of non-allelic gene action,

j = measures additive x dominance type of non-allelic gene action,

l = measures dominance x dominance type of non-allelic gene action.

The estimates of m, d, h, i, j and l were made following a weighted least square technique as described under 3-parameter model.

As we have eight generations and six estimates, we can test the adequacy of the model by a X^2 with 2 d.f. The X^2 was calculated in the same way as it was done for 3-parameter model.

Components of Variation:

The variances of segregating generations viz. F_2, F_3, F_4, B_1 and B_2 generations consist of heritable and non-heritable components. The heritable component consist of fixable heritable (D) and non-fixable heritable (H) types of variation. Variation in the non-segregating generations viz. P_1,P_2 and F_1 are non-heritable in nature.

From the eight generations ($P_1, P_2, F_1, F_2, F_3, F_4, B_1$ and B_2) twelve different types of variances and covariances were calculated and they are,

VF_2, $F_1\bar{F}_3$, $\bar{V}_2F_3$, $WF_3/\bar{F}_2$, F_1F_4, V_2F_4, V_3F_4, W_1F_3/F_4 W_2F_3/F_4, VE_1, VE_2 and $VB_1 + VB_2$.

The composition of those variances in terms of heritable and non-heritable components of variation were as follows:

$$VF_2 = \tfrac{1}{2}D + \tfrac{1}{4}H + E_1$$
$$V_1\bar{F}_3 = \tfrac{1}{2}D + 1/_{16}H + E_2$$
$$\bar{V}_2F_3 = \tfrac{1}{4}D + 1/_8H + E_1$$
$$WF_3/\bar{F}_2 = \tfrac{1}{2}D + 1/_8H$$
$$V_1F_4 = \tfrac{1}{2}D + 1/_{64}H$$
$$V_2F_4 = \tfrac{1}{4}D + 1/_{32}H + E_2$$
$$V_3F_4 = 1/_8D + 1/_{16}H + E_1$$
$$W_1F_3/F_4 = \tfrac{1}{2}D + 1/_{32}H$$
$$W_2F_3/F_4 = \tfrac{1}{4}D + 1/_{16}H$$
$$VE_1 = E_1$$
$$VE_2 = E_2$$
$$VB_1 + VB_2 = \tfrac{1}{2}D + \tfrac{1}{2}H + 2E_1$$

The non-heritable components of variation in a generation were found out from the variances of non segregating generations

as follows:

$$E_1 = \frac{1}{4}VP_1 + \frac{1}{4}VP_2 + \frac{1}{2}VF_1$$

E_1 measures the non-heritable variances of individual, E_2 measures the non-heritable variances of F_3 and F_4 family means. In general E_2 is lesser than E_1 because each family means is based on 'n' number of individuals and it will be $(1/_n)$ E_1 where the differences in environment between individual in different families were not greater than those to which members of the same family were subjected. Therefore, E_2 was measured as follows:

$$E_2 = E_1/\text{ (harmonic mean number per } F_3 \text{ families)}$$

The twelve equations obtained from the segregating and non-segregating generations were subjected to a least square technique of analysis for the estimation of components of variation D, H, E_1 and E_2. Unweighted least square techniques developed by Mather (1949) and Mather and Jink (1971) were followed. Components of variation when estimated using all the twelve equation were termed as inclusive estimates while these components when estimated excluding $\bar{V}_2F_3$, V_2F_4, V_3F_4 termed as exclusive estimates.

<u>Inclusive Analysis:</u>

The twelve equations mentioned in the preceding paragraphs contained four unknown which were estimated by

unweighted least square technique.

In the first step of analysis the twelve equations were combined to form four normal equations yielding least square estimates for four components (D, H, E_1 and E_2). Each of the twelve equations was multiplied through by the coefficient of D which it contained and the equations were then summed omitting those which did not include D. The three other equations were also found out similarly but using the coefficients of H, E_1 and E_2 as multipliers in turn. The four equation thus obtained were as follows:

(1) $1.7283\ D + 0.5596\ H + 1.9056\ E_1 + 0.7906\ E_2$

(2) $0.5596\ D + 0.3585\ H + 1.4415\ E_1 + 0.1021\ E_2$

(3) $1.9056\ D + 1.4415\ H + 8.0032\ E_1 + 0.08\ E_2$

(4) $0.7906\ D + 0.1021\ H + 0.08\ E_1 + 3.0025\ E_2$

By solving these four sets of equations a matrix of multipliers was obtained of which C_{DD} was the value of D in the first of the four sets and C_{DH}, C_{DE_1} and C_{DE_2}, the value of D in the second, third and fourth sets respectively. Similarly C_{HD}, C_{HH}, C_{HE_1} and C_{HE_2} were the values of H in the four sets and so on. This matrix turns out to be as shown in page 72

In the second step the observed values of twelve equations were multiplied by the corresponding coefficient of D which it contained and was summed which denoted as $S_{(DY)}$. Similarly $S_{(HY)}$, $S_{(E_1Y)}$ and $S_{(E_2Y)}$ were calculated by using the coefficient of H, E_1 and E_2 as multiplier in turn. The unweighted least square estimate of D was then found in the following way using the D column of the page 72.

$$D = C_{DD} \times S_{(DY)} + C_{DH} \times S_{HY)} + C_{DE_1} \times S_{(E_1Y)} + C_{DE_2} \times S_{(E_2Y)}$$

Similarly, H, E_1 and E_2 were calculated from the H, E_1 and E_2 column respectively of page 72 as follows:

$$H = C_{DH} \times S_{DY)} + C_{HH} \times S_{HY)} + C_{HE_1} \times S_{(E_1Y)} + C_{HE_2} \times S_{(E_2Y)}.$$

$$E_1 = C_{DE_1} \times S_{(DY)} + C_{HE_1} \times S_{(HY)} + C_{E_1E_1} \times S_{(E_1Y)} + C_{E_1E_2} \times S_{(E_2Y)}$$

$$E_2 = C_{DF_2} \times S_{(DY)} + C_{HE_2} \times S_{(HY)} + C_{E_1E_2} \times S_{(E_1Y)} + C_{E_2E_2} \times S_{(E_2Y)}$$

The estimated D, H, E_1 and E_2 values were put in the twelve equations to get expected values of the equations. Then the deviation of the observed value from the expected value of each of the twelve equations were found out. The twelve deviations one for each statistics were squared and then summed which gave sum of the deviation square ($Dev.^2$).

The standard error of D, H, E_1 and E_2 were calculated from Dev.^{2} obtained from the twelve equations, the Dev.^{2} of the four replications were added and divided by 16 (total item) to get Dev.m.s. The values thus obtained were used to calculate the standard errors of four components of variations obtained from the over all estimates as follows:

$$\text{S.E. of D} = \tfrac{1}{4}(\text{Dev. m.s.} \times C_{DD})^{\frac{1}{2}}$$

$$\text{S.E. of H} = \tfrac{1}{4}(\text{Dev. m.s.} \times C_{HH})^{\frac{1}{2}}$$

$$\text{S.E. of } E_1 = \tfrac{1}{4}(\text{Dev. m.s.} \times C_{E_1E_1})^{\frac{1}{2}}$$

$$\text{S.E. of } E_2 = \tfrac{1}{4}(\text{Dev. m.s.} \times C_{E_2E_2})^{\frac{1}{2}}$$

Inverse matrix of inclusive analysis used in the estimation of components of variation is as follows:

	D	H	E_1	E_2
D	C_{DD} 1.4574	C_{DH} -2.9335	C_{DE_1} 0.1842	C_{DE_2} -0.2889
H	C_{DH} -2.9335	C_{HH} 16.2885	C_{HE_1} -2.2381	C_{HE_2} 0.2781
E_1	C_{DE_1} 0.1842	C_{HE_1} -2.2381	$C_{E_1E_1}$ 0.4840	$C_{E_1E_2}$ 0.0146
E_2	C_{DE_2} -0.2889	C_{HE_2} 0.2781	$C_{E_1E_2}$ 0.0146	$C_{E_2E_2}$ 0.3992

<u>Exclusive Analysis:</u>

The least square estimates of D, H, E_1 and E_2 were performed exactly in the same way as mentioned under

inclusive analysis but here the rank 2 statistics (V_2F_3, V_2F_4 and V_3F_4) was excluded. Thus there were nine equations for the estimation of D, H, E_1 and E_2.

The nine equations were condensed to form four equations for the least square estimates for the four components (D, H, E_1 and E_2) and they were as mentioned below:

(1) $1.5852\ D + 0.5119\ H + 1.5204\ E_1 + 0.5356\ E_2$

(2) $0.5119\ D + 0.3378\ H + 1.2527\ E_1 + 0.0683\ E_2$

(3) $1.5204\ D + 1.2527\ H + 6.0016\ E_1 + 0.04\ E_2$

(4) $0.5356\ D + 0.0683\ H + 0.04\ E_1 + 2.0025\ E_2$

The matrix multipliers (inverse matrix) which obtained for exclusive estimates of D, H, E_1 and E_2 are shown in page 74

The values of $S_{(DY)}$, $S_{(HY)}$, $S_{(E_1Y)}$ and $S_{(E_2Y)}$ are obtained using the same procedure as described under inclusive analysis. The unweighted least square estimates of D, H, E_1 and E_2 were then calculated from respective column of page 74 as follows:

$$D = C_{DD} \times S_{(DY)} + C_{DH} \times S_{(HY)} + C_{DE_1} \times S_{(E_1Y)} + C_{DE_2} \times S_{(E_2Y)}$$

$$H = C_{DH} \times S_{(DY)} + C_{HH} \times S_{HY)} + C_{HE_1} \times S_{(E_1Y)} + C_{HE_2} \times S_{(E_2Y)}.$$

$$E_1 = C_{DE_1} \times S_{(DY)} + C_{HE_1} \times S_{(HY)} + C_{E_1E_1} \times S_{(E_1Y)} + C_{E_1E_2} \times S_{(E_2Y)}$$

$$E_2 = C_{DE_2} \times S_{(DY)} + C_{HE_2} \times S_{(HY)} + C_{E_1E_2} \times S_{(E_1Y)} + C_{E_2E_2} \times S_{(E_2Y)}.$$

The estimated values D, H, E_1 and E_2 were put in the nine equations to get expected values of nine equations in terms of the estimated D, H, E_1 and E_2.

The standard errors of the components were calculated exactly in the same way as those described under inclusive analysis. Inverse matrix of exclusive analysis used in the estimation of components of variation is as follows:

D	C_{DD}	1.5794	C_{DH}	-3.7895	C_{DE_1}	0.3928	C_{DE_2}	-0.3010
H	C_{DH}	-3.7895	C_{HH}	22.5089	C_{HE_1}	-3.7403	C_{HE_2}	0.3205
E_1	C_{DE_1}	0.3928	C_{HE_1}	-3.7403	$C_{E_1E_1}$	0.8477	$C_{E_1E_2}$	0.0055
E_2	C_{DE_2}	-0.3010	C_{HE_2}	0.3205	$C_{E_1E_2}$	0.0055	$C_{E_2E_2}$	0.5688

Number of Effective Factor:

The number of effective factor was estimated in four different ways as follows:

(i) Castle and Wright (1921) presented the formula for the estimation of minimum number of factors or genes controlling a character. According to them the possible number of effective gene groups is estimated by dividing the square of the difference of the two parental means with the difference of variances of F_2 and F_1 multiplied by eight.

$$\text{Thus } n_1 = \frac{(\bar{P}_1 - \bar{P}_2)^2}{8(VF_2 - VF_1)}$$

(ii) According to Mather (1949) gave the formula for estimating the possible number of effective gene groups controlling a character as follows:

$$K_1 = (\tfrac{1}{2} \bar{P}_1 - \tfrac{1}{2}\bar{P}_2)^2 /D$$

where, D = least square estimate of component of genetic variation.

(iii) Mather (1949) also gave another approach of estimating the number of effective factors controlling a character as follows:

$$K_2 = H\bar{V}F_3 \; / \; (V_{VF_3} - C \;)$$

where $H\bar{V}_{F_3}$ is the heritable mean variance of F_3 families and and C is the correction factor for $V_{V_{F_3}}$ obtained by dividing $2\bar{V}_{F_3}^{2}$ with the harmonic mean number of seedlings per F_3 families.

(iv) According to Burton (1951) estimation of effective factor was made as follows:

$$n_2 = \frac{0.25\ (0.75 - h + h^2)\ D^2}{(VF_2 - VF_1\ )}$$

where, $D = \bar{P}_2 - \bar{P}_1$ ($\bar{P}_1$ always the smaller parent) and

$$h = (\bar{F}_1 - \bar{P}_1) / (\bar{P}_2 - \bar{P}_1)$$

Heritability:

Heritability was calculated in two different ways as follows:

(i) Broad sense Heritability: It was expressed as the ratio of genotype variance over the (expected) phenotypic variance of the F_2 generations, as follows:

$$\text{Heritability (Broad sense)} = (\tfrac{1}{2}D+\tfrac{1}{4}H)/(\tfrac{1}{2}D+\tfrac{1}{4}H+E_1)$$

(ii) Narrow sense Heritability: It was expressed as the ratio of fixable heritable variation (D) over the (expected) phenotypic variance of the F_2 generation as follows:

Heritability (Narrow Sense) = $\frac{1}{2}D/(\frac{1}{2}D + \frac{1}{4}H + E_1)$

where the D, H and E_1 are the least square estimate of components of variation.

Degree of Dominance:

Degree of dominance was calculated following two methods.

(i) Dominance Ratio Method: The average degree of dominance over two loci was determined by the square root of the ratio between H and D (Mather, 1949), where

$(H/D)^{\frac{1}{2}}$ = 0, denotes no dominance

$(H/D)^{\frac{1}{2}}$ = 1, denotes complete dominance

$(H/D)^{\frac{1}{2}} < 1$, denotes partial dominance

$(H/D)^{\frac{1}{2}} > 1$, denotes over-dominance

D and H are the least square estimate of components of variation.

(ii) Potence Ratio Method: Degree of dominance in F_1, F_2, F_3 and F_4 generations were calculated as described by Petr and Frey (1966) as follows:

Degree of dominance in $F_1 = h_1 = (\bar{F}_1 - \overline{MP})/(\overline{HP} - \overline{MP})$,

Degree of dominance in $F_2 = h_2 = 2(\bar{F}_2 - \overline{MP})/(\overline{HP} - \overline{MP})$,

Degree of dominance in $F_3 = h_3 = 4\ (\bar{F}_3 - \overline{MP})/(\overline{HP} - \overline{MP})$,

Degree of dominance in $F_4 = h_4 = 8(\bar{F}_4 - \overline{MP})/(\overline{HP} - \overline{MP})$

where MP is the mid parent and HP is the higher parent.

RESULTS

The results obtained from each of the eight experiments have been described separately as follows:

Experiment 1:

Twelve genotypes collected from the Department of Botany, were evaluated in respect of genotype-environment interaction shown by coleoptile length grown under five different temperatures. The temperatures under which the seedling were raised were treated as environment. The genotypic mean of the twelve genotypes over five different environments are shown in table 1. This experiment was repeated in seven conjugative years starting from 1976 and continuing upto 1982. Genotypic means performed differently for different environments but a close agreement between years was shown by correlation coefficient of mean coleoptile length in seven years (1976 to 1982). These were high and highly significant (column 1, table 9). A considerable range of variation was observed among the genotypes included in this study. Lowest coleoptile length was seen in Sonora- 64, whereas highest coleoptile length was noted in Kazoli. Analysis of variance as shown in table 3 indicated that highly significant differences in coleoptile length exist among the genotypes included in this study.

Significant effects of temperature on coleoptile length were also noted as revealed by the analysis of variance (Table 3). The over all mean of the twelve genotypes in each of the five different temperature are shown in table 2. Highest coleoptile length was obtained at 40°C, whereas the lowest was obtained at 20°C. A close agreement in the result obtained in seven years as the correlation coefficient were very high and highly significant (column 2, table 9).

The analysis of variance also indicated that a significant part of the total variation was due to genotype-environment interaction effects. This result was highly significant in all the seven years.

The item replication was non-significant suggesting that one part of the experiment was the same as those of the other parts.

The estimates of the variances for genotypes, $\delta^2 g$, environments, δ^2_e, genotype x environment, $\delta^2 g$ x e, and within genotypes and environments (between individuals), δ^2_w as, derived from an analysis of variance (table 3) are given in table 4. The two main effects and their interaction are highly significant in the seven years study. The genotype-environmental interaction effects were consistently high in all the seven years suggesting importance of genotype-environment interaction effects in the expression of coleoptile length of wheat.

Additive genetical components, (d_i), for different genotypes in different years are shown in table 6. These genetical components were found to be similar in different years. It was highest in Sonora- 64 and lowest in Kazoli.

Since the interactions item are significant, no immediate generalisation can be made on the relative performance of these populations, but the analysis shows that valid comparisons can only be made in each environment separately.

Since the analysis of variance can give no further useful account of the genotype-environment interactions, we can now consider any dynamic relationship which exist between genotypic and environmental effects in the method proposed by Finlay and Wilkinson (1963).

The genotype-environmental interactions of these genotypes were investigated for linearity by regressing their performance in each environment against a biological measure of the environments. The performance of each of the twelve genotypes was regressed against the mean of all the genotypes in each environment, i.e. the material used for the environmental assessment is the same as that to be investigated. This environmental measurement will be termed dependent ej. The dependent ej values are shown in table 5. The assessment of the ej values are very similiar in all the seven years study.

For each genotype the linear regression of individual values on these five environmental means (ej) were computed (table 7). Following this, the sum of squares measuring the interactions of the genotypes with environments were repartitioned into an item measuring differences between the slopes of the five regressions and a residual item which measures the scatter of points about the regression lines. The results of this analysis are also given in table 3. It is immediately clear that the major part of the genotype x environment variance is explained by differences between the slopes of linear regression. The deviations mean square is significantly greater than the replicates error item that suggested there are deviations from linearity which cannot be explained in terms of field error.

The regression coefficients (b) in table 7 correspond to the b values of Finlay and Wilkinson, (1963), and to the ($1+\beta i$) values of Eberhart and Russell (1966); after subtracting 1.0 they correspond with the β_i (table 8) values of Perkins and Jinks (1968a). The actual regression lines of performances of the genotypes against the corresponding environmental means are shown in fig. 1. In order to avoid confusion, individual points were not plotted in the figures. Marked crossing of the regression lines is one of the common features of the graph in all the seven years study. The genotypic differences were very marked in high temperatures compared to low temperatures.

The regression firstly measures response to increments in an improving environments. Since these increments are measured by the mean of all genotypes, then the average response for any set of genotypes under consideration must have a regression coefficient of 1.0. Regression coefficient < 1.0 and >1.0 indicate below and above average response respectively by a variety of any set of genotypes under consideration. The distribution of the values of regression coefficient (b) of seven years study of the twelve genotypes (table 7) were heterogeneus, hence all the genotypes have different response to the different environments.

The regression coefficient with standard error are shown in table 7. Mexipak- 65, Innia- 66, Norteno- 67, Jupatica- 70, Penkty and Kazoli had an above average response in all the seven years study and was consistently the highest coleoptile length in all above average environments. Sonora- 64, Sonalika, Tanori- 71, Noori, Janak, and Dirk, on the other hand, has a response below the average and showed lowest coleoptile length to the environments in the seven years studied. Penkty showed highest coleoptile length to the environments and is marked by a high response (b = 1.82, 1.56, 1.79, 1.83, 1.61, 1.89 and 1.92) respectively, but a comparatively low mean coleoptile in this range of environment in all the seven years study.

The standard errors attached to the regression coefficient in table 7 have been calculated separately for each linear regression from deviations within the twelve genotypes. They are very variable and reflect the fact that mean squares measuring the scatter of points about individual regression lines are not homogenous. The Chi-square (χ^2) in the Bertle-tts test was highly significant in all the seven years study. It suggested that the extent of the deviations from regre-ssion is specific to, and hence characteristic of, particular genotypes. It must be emphasised that in no case did the graphs indicate any relationship other than linear, individual points being scattered at random about the fitted straight line. Standard error measuring this scatter may thus be taken as measures of the "stability of response" exhibited by each genotype. The phenotypic expression of a particular genotype in a specific environments depends on three genotypic properties: a mean expression, a linear response to environment and residual deviations from regression. These parameters are exactly those proposed by Eberhart and Russell, (1966), which measure the unpredictable irregularities in the responses to the environments of the twelve genotypes in seven years results. These are also shown in table 7. The S_b values were highly heterogenous in most of the twelve genotypes as revealed in joint regression and standard error of regression. The S_b values were proved to be heterogenous as the χ^2 was highly

significant (χ^2 = 58.03, 15.24, 51.18, 34.91, 44.26, 30.44 and 36.56). Among the twelve genotypes, Sonora- 64, Tanori- 71, Noori, Janak and Dirk were the most stable genotypes as shown by their low S_b values whereas, Mexipak-65 showed least stability in all the seven years study of the results.

Evaluation of these genotypes in terms of linearity were also investigated by using independent environmental values. They are given below:

(a) Independent Z_j using replicate individuals:

Each genotype in each environment was represented by ten individual seedlings. These were split at random into two groups of five, the interactions of one group were to be investigated and the other group contributed to the environmental assessment.

(b) Independent Z_j using replicate sets of genotypes:

The twelve genotypes were divided at random into two sets of six, the interactions of one set were to be investigated and the other set were to assess the environment.

Group (a) and (b) were further divided into sub-groups $(a)_i$ and $(a)_{ii}$ and $(b)_i$ and $(b)_{ii}$. Subgroups $(a)_i$ and $(a)_{ii}$ represent the regression of the twelve genotypes in one set of replicate individuals against the mean of the other set in

each environment and vice versa. Similarly, subgroups $(b)_i$ and $(b)_{ii}$ represent the regression of the six genotypes in one set against the mean of the other set in each environment and vice versa.

We try to use independent environmental assessment as a measure of environmental values and the results obtained by using independent environmental values are shown in table 10 and 11. A good agreement of the result was obtained from different independent Z_j assessment with that of dependent ej assessment. The joint remainder of table 10 was non-significant when tested against the variance within genotypes and environments (between individuals). The joint regression coefficient $\bar{\beta}$, should not deviate from one. This result was found to be similar in all the seven years studied.

In table 11 the significance of the heterogeneity of regression and of the heterogeneity of remainders in the joint regression analysis of the twelve genotypes against the different kinds of independent environmental assessors are given for each year. The heterogeneity of remainders was tested against the variance within genotypes and environments (between individuals). The heterogeneity of regression was also tested against the variance within genotypes and environments. The results are completely consistent across all the different ways of assessing the independent environment with those of dependent environments.

Table 1: Genotypic mean.

Genotypes	1976	1977	1978	1979	1980	1981	1982
1. Sonora-64	52.17	54.17	53.76	50.21	52.79	52.11	53.62
2. Mexipak-65	55.23	56.29	52.11	54.29	55.07	55.46	54.23
3. Innia-66	61.19	60.55	62.32	61.14	60.59	62.73	61.55
4. Norteno-67	67.74	66.32	68.29	63.63	65.30	67.19	68.32
5. Sonalika	53.65	52.06	54.05	53.93	53.64	52.84	55.05
6. Tanori-71	58.95	59.32	60.23	58.66	57.32	58.90	58.47
7. Hupatica-70	62.23	64.62	60.05	60.09	61.44	62.30	62.80
8. Noori	59.25	57.17	60.22	58.29	59.74	60.04	58.82
9. Penkti	64.67	63.22	63.32	63.29	62.92	64.02	64.09
10. Janak	62.19	60.05	60.55	62.82	63.70	62.65	61.95
11. Dirk	72.36	70.36	69.32	70.24	70.75	73.19	73.05
12. Kazoli	82.15	81.36	80.04	80.53	81.09	82.55	81.46

Table 2: Population mean.

	20°C	25°C	30°C	35°C	40°C	Mean
1976	55.17	64.24	58.32	64.15	71.11	62.59
1977	51.29	63.04	54.10	66.39	75.32	62.02
1978	53.22	62.29	57.74	63.33	70.75	61.46
1979	49.23	60.13	55.22	62.19	73.75	60.10
1980	53.04	64.12	59.22	65.17	68.32	61.97
1981	55.14	63.65	57.49	65.23	72.05	62.71
1982	54.36	65.19	56.34	62.82	73.89	62.52

Table 3: Results of analysis of variance (m.s.)

Item	d.f	1976	1977	1978	1979	1980	1981	1982
Temperature (E)	4	151.03***	405.01***	172.22***	332.66***	142.49***	179.02***	241.27***
Genotype(G)	11	282.97***	253.94***	240.56***	256.43***	250.05***	306.31***	269.06***
G x E	44	121.64***	154.22***	87.65***	129.33***	167.73***	214.15***	159.73***
Regression	11	164.76***	147.29***	54.29***	179.04***	204.76***	195.32***	169.44***
Remainder	33	115.27***	156.53***	98.77***	112.76***	155.39***	220.43***	156.49***
Reps. in E	15	14.73	29.64	18.23	4.19	11.05	10.36	11.15
Error	165	20.34	26.36	14.23	30.19	18.36	9.23	18.64

*** Significant at 0.1% level.

Table 4: Estimates of variance components.

Components	1976	1977	1978	1979	1980	1981	1982
Genotypes $\delta^2 g$	7.76	4.98	7.64	6.35	4.11	4.61	5.46
Environments $\delta^2 e$ (Temp.)	2.72	7.88	3.29	6.30	2.58	3.53	4.63
Genotypes x environments $\delta^2 ge$	26.82	31.96	18.35	24.78	37.34	51.23	35.27
Within Genotypes and environments δ^2_{ws}	20.34	26.36	14.23	30.19	18.36	9.23	18.64

Table 5: Environmental values (ej)

	20°C	25°C	30°C	35°C	40°C
1976	7.42	-1.65	4.27	-1.56	-8.52
1977	10.73	-1.02	7.92	-4.37	-13.30
1978	8.24	-0.83	3.72	-1.87	-9.29
1979	10.87	-0.03	4.88	-2.09	-13.65
1980	8.93	-2.15	2.75	-3.20	-6.35
1981	7.57	-0.94	5.22	-2.52	-9.34
1982	8.16	-2.67	6.18	-0.30	-11.37

Table 6: Additive genetical components, (d_i)

Genotypes	1976	1977	1978	1979	1980	1981	1982
1 Sonora-64	10.47	7.94	8.26	11.21	9.24	10.55	9.16
2 Mexipak-65	7.41	5.82	9.91	7.13	6.96	7.20	8.55
3 Innia-66	1.45	1.56	-0.30	0.28	1.44	-0.07	1.23
4 Norteno-67	5.10	4.21	-6.27	-2.21	-3.27	-4.53	-5.54
5. Sonalika	8.99	10.05	7.97	7.49	8.39	9.82	7.73
6 Tanori-71	3.69	2.79	1.79	2.76	4.71	3.76	4.31
7 Jupatika	0.41	-2.51	1.97	1.33	0.59	0.36	-0.02
8 Noori	3.39	4.94	1.80	3.13	2.29	2.62	3.96
9 Penkty	-2.03	-1.11	-1.30	-1.87	-0.89	-1.36	-1.31
10 Janak	0.45	2.06	1.47	-1.40	-1.67	0.01	0.83
11 Dirk	-9.72	-8.25	-7.30	-8.82	-8.72	-10.53	-10.27
12 Kazoli	-19.51	-19.19	-18.02	-19.11	-19.06	-19.89	-18.68

Table 7: Regression co-efficients with standard errors.

Genotypes	1976	1977	1978	1979	1980	1981	1982
1. Sonora-64	0.49 $\pm$ 0.03	0.83 $\pm$ 0.19	0.56 $\pm$ 0.14	0.44 $\pm$ 0.22	0.50 $\pm$ 0.06	0.48 $\pm$ 0.21	0.42 $\pm$ 0.13
2. Mexipak-65	1.59 $\pm$ 0.64	1.76 $\pm$ 0.29	1.82 $\pm$ 0.76	1.64 $\pm$ 0.44	1.72 $\pm$ 0.55	1.82 $\pm$ 0.39	1.44 $\pm$ 0.41
3. Innia-66	1.04 $\pm$ 0.23	0.89 $\pm$ 0.14	0.94 $\pm$ 0.16	1.11 $\pm$ 0.22	0.95 $\pm$ 0.19	1.06 $\pm$ 0.22	0.93 $\pm$ 0.07
4. Norteno-67	1.22 $\pm$ 0.36	1.26 $\pm$ 0.39	1.19 $\pm$ 0.16	1.34 $\pm$ 0.22	1.05 $\pm$ 0.14	1.19 $\pm$ 0.32	1.26 $\pm$ 0.11
5. Sonalika	0.54 $\pm$ 0.19	0.44 $\pm$ 0.10	0.55 $\pm$ 0.11	0.58 $\pm$ 0.16	0.60 $\pm$ 0.07	0.49 $\pm$ 0.03	0.51 $\pm$ 0.15
6. Tanori-71	0.82 $\pm$ 0.04	0.76 $\pm$ 0.19	0.82 $\pm$ 0.13	0.94 $\pm$ 0.22	0.82 $\pm$ 0.16	0.89 $\pm$ 0.14	0.80 $\pm$ 0.07
7. Jupatica-70	1.57 $\pm$ 0.32	1.69 $\pm$ 0.27	1.50 $\pm$ 0.31	1.52 $\pm$ 0.44	1.84 $\pm$ 0.41	1.65 $\pm$ 0.26	1.69 $\pm$ 0.22
8. Noori	0.45 $\pm$ 0.09	0.46 $\pm$ 0.11	0.40 $\pm$ 0.04	0.32 $\pm$ 0.11	0.49 $\pm$ 0.15	0.41 $\pm$ 0.16	0.44 $\pm$ 0.07
9. Penkty	1.82 $\pm$ 0.49	1.56 $\pm$ 0.22	1.79 $\pm$ 0.31	1.83 $\pm$ 0.71	1.61 $\pm$ 0.62	1.89 $\pm$ 0.44	1.92 $\pm$ 0.14
10. Janak	0.95 $\pm$ 0.22	0.72 $\pm$ 0.16	0.92 $\pm$ 0.07	0.98 $\pm$ 0.19	0.96 $\pm$ 0.27	0.90 $\pm$ 0.34	0.94 $\pm$ 0.05
11. Dirk	0.47 $\pm$ 0.07	0.49 $\pm$ 0.14	0.55 $\pm$ 0.19	0.36 $\pm$ 0.07	0.44 $\pm$ 0.14	0.49 $\pm$ 0.07	0.52 $\pm$ 0.22
12. Kazoli	0.99 $\pm$ 0.12	1.14 $\pm$ 0.14	0.96 $\pm$ 0.22	0.94 $\pm$ 0.16	1.02 $\pm$ 0.15	0.73 $\pm$ 0.22	1.13 $\pm$ 0.33
χ^2 = (d.f.11)	58.03***	15.24	51.18***	34.91***	44.26***	30.44**	36.56***

, * Significant at 1% and 0.1% level respectively.

Table 8: Linear interaction co-efficients, (β_i).

Genotypes	1976	1977	1978	1979	1980	1981	1982
1. Sonora-64	-0.51	-0.17	-0.44	-0.56	-0.5	-0.52	-0.58
2. Mexipak-65	0.59	0.76	0.82	0.64	0.72	0.82	0.44
3. Innia-66	0.04	-0.11	-0.06	0.11	-0.05	0.06	-0.07
4. Norteno-67	0.22	0.26	0.19	0.34	0.05	0.19	0.26
5. Sonalika	-0.46	-0.36	-0.45	-0.42	-0.40	-0.51	-0.49
6. Tanori-71	-0.13	-0.24	-0.18	-0.06	-0.18	-0.11	-0.20
7. Jupatica-70	0.57	0.69	0.50	0.52	0.84	0.65	0.69
8. Noori	-0.55	-0.54	-0.60	-0.68	-0.51	-0.59	-0.56
9. Penkty	0.82	0.76	0.79	0.83	0.61	0.89	0.92
10. Janak	-0.05	-0.18	-0.08	-0.02	-0.04	-0.10	-0.06
11. Dirk	-0.53	-0.51	-0.45	-0.64	-0.56	-0.51	-0.48
12. Kazoli	-0.01	0.14	-0.04	-0.06	0.02	-0.07	0.13

Table 9: Correlation studies.

	Between Genotypic mean	Between Population mean	Between Regression co-efficients
1976 vs. 1977	0.9823	0.9886	0.9543
78	0.9790	0.9949	0.9828
79	0.9885	0.9864	0.9904
80	0.9918	0.9589	0.9649
81	0.9969	0.9944	0.9929
82	0.9954	0.9884	0.9837
1977 vs. 1978	0.9544	0.9856	0.9684
79	0.9604	0.9797	0.9328
80	0.9703	0.9442	0.9564
81	0.9789	0.9988	0.9581
82	0.9784	0.9701	0.9422
1978 vs. 1979	0.9648	0.9962	0.9715
80	0.9663	0.7611	0.9452
81	0.9764	0.9912	0.9927
82	0.9799	0.9744	0.9527
1979 vs. 1980	0.9905	0.9316	0.9412
81	0.9897	0.9857	0.8036
82	0.9790	0.9698	0.9614
1980 vs. 1981	0.9929	0.9476	0.9698
82	0.9863	0.9101	0.9488
1981 vs. 1982	0.9913	0.9791	0.9637

Table 10: Testing the adequacy of the independent environmental assessors $(a)_i$, $(a)_{ii}$ and $(b)_i$ and $(b)_{ii}$ from the significance of joint regression, $\bar{\beta}$ from one and of the joint remainder.

Item	d.f.	$(a)_i$	$(a)_{ii}$	d.f.	$(b)_i$	$(b)_{ii}$
			1976			
$\bar{\beta}$		0.97	1.04		0.99	0.94
$\bar{\beta}-1$		-0.03	0.04		-0.01	-0.06
Joint Remainder	3	14.76	21.05	3	11.16	6.94
Error	165	19.76	17.36	85	17.94	21.55
			1977			
$\bar{\beta}$		0.94	0.97		0.89	1.07
$\bar{\beta}-1$		-0.06	-0.03		-0.11	0.07
Joint Remainder	3	14.55	19.36	3	27.04	21.59
Error	165	21.44	16.75	85	29.13	27.54
			1978			
$\bar{\beta}$		0.99	0.96		0.87	0.95
$\bar{\beta}-1$		-0.01	-0.04		-0.13	-0.05
Joint Remainder	3	11.67	16.94	3	12.32	7.69
Error	165	11.76	16.73	85	14.22	12.32
			1979			
$\bar{\beta}$		0.94	0.93		0.99	0.99
$\bar{\beta}-1$		-0.06	-0.07		-0.01	-0.01
Joint Remainder	3	34.63	21.53	3	29.23	36.75
Error	165	34.73	29.73	85	31.14	27.16
			1980			
$\bar{\beta}$		0.79	0.88		0.94	0.93
$\bar{\beta}-1$		-0.21	-0.12		-0.06	-0.07
Joint Remainder	3	24.76	20.19	3	11.55	14.73
Error	165	21.14	26.95	85	17.75	19.32
			1981			
$\bar{\beta}$		0.95	0.81		0.64	0.95
$\bar{\beta}-1$		-0.05	-0.19		-0.36	-0.05
Joint Remainder	3	11.23	4.39	3	4.04	9.16
Error	165	11.14	12.64	85	7.93	9.13
			1982			
$\bar{\beta}$		0.99	0.91		0.74	0.76
$\bar{\beta}-1$		-0.01	-0.09		-0.26	-0.24
Joint Remainder	3	21.45	19.66	3	27.23	29.11
Error	165	19.75	20.10	85	24.23	21.55

Table 11: Significance of heterogeneity of remainder using the environmental assessors $(a)_i$, $(a)_{ii}$, $(b)_i$ and $(b)_{ii}$.

Item	d.f.	$(a)_i$	$(a)_{ii}$	d.f.	$(b)_i$	$(b)_{ii}$
1976						
Heterogeneity of Regression	11	141.32***	169.70***	5	115.76***	145.05***
Heterogeneity of Remainder	33	92.36***	114.32***	15	99.73***	124.76***
Error	165	19.76	17.36	85	17.94	21.55
1977						
Heterogeneity of Regression	11	124.66***	97.64***	5	155.27***	224.66***
Heterogeneity of Remainder	33	119.73***	104.32***	15	114.19***	174.39***
Error	165	21.44	16.75	85	29.13	27.54
1978						
Heterogeneity of Regression	11	69.73***	126.73***	5	104.41***	93.29***
Heterogeneity of Remainder	33	62.30***	69.55***	15	60.55***	71.24***
Error	165	11.76	16.73	85	14.22	12.32
1979						
Heterogeneity of Regression	11	207.16***	116.75***	5	197.67***	214.93***
Heterogeneity of Remainder	33	94.44***	103.58***	15	81.35***	49.73***
Error	165	34.73	29.73	85	31.14	27.16
1980						
Heterogeneity of Regression	11	201.06***	295.64***	5	106.73***	181.51***
Heterogeneity of Remainder	33	116.05***	205.11***	15	54.21***	106.37***
Error	165	21.14	26.95	85	17.75	19.32

(contd.)

Table 11: (contd.)

Item	d.f.	$(a)_i$	$(a)_{ii}$	d.f.	$(b)_i$	$(b)_{ii}$
1981						
Heterogeneity of Regression	11	224.76***	190.50***	5	239.55***	109.15***
Heterogeneity of Remainder	33	206.07***	187.74***	15	106.74***	94.32***
Error	165	11.14	12.64	85	7.93	9.23
1982						
Heterogeneity of Regression	11	184.32***	161.65***	5	214.09***	183.76***
Heterogeneity of Remainder	33	129.64***	155.03***	15	191.82***	105.33***
Error	165	19.75	20.10	85	24.23	21.55

*** Significant at 0.1% level.

Fig. 1: Phenotypic regressions of coleoptile length for different genotypes against environment (Temperature) means.

1. Sonora- 64
2. Mexipak- 65
3. Innia- 66
4. Norteno- 67
5. Sonalika
6. Tanori- 71
7. Jupatica- 70
8. Noori
9. Penkty
10. Janak
11. Dirk
12. Kazoli

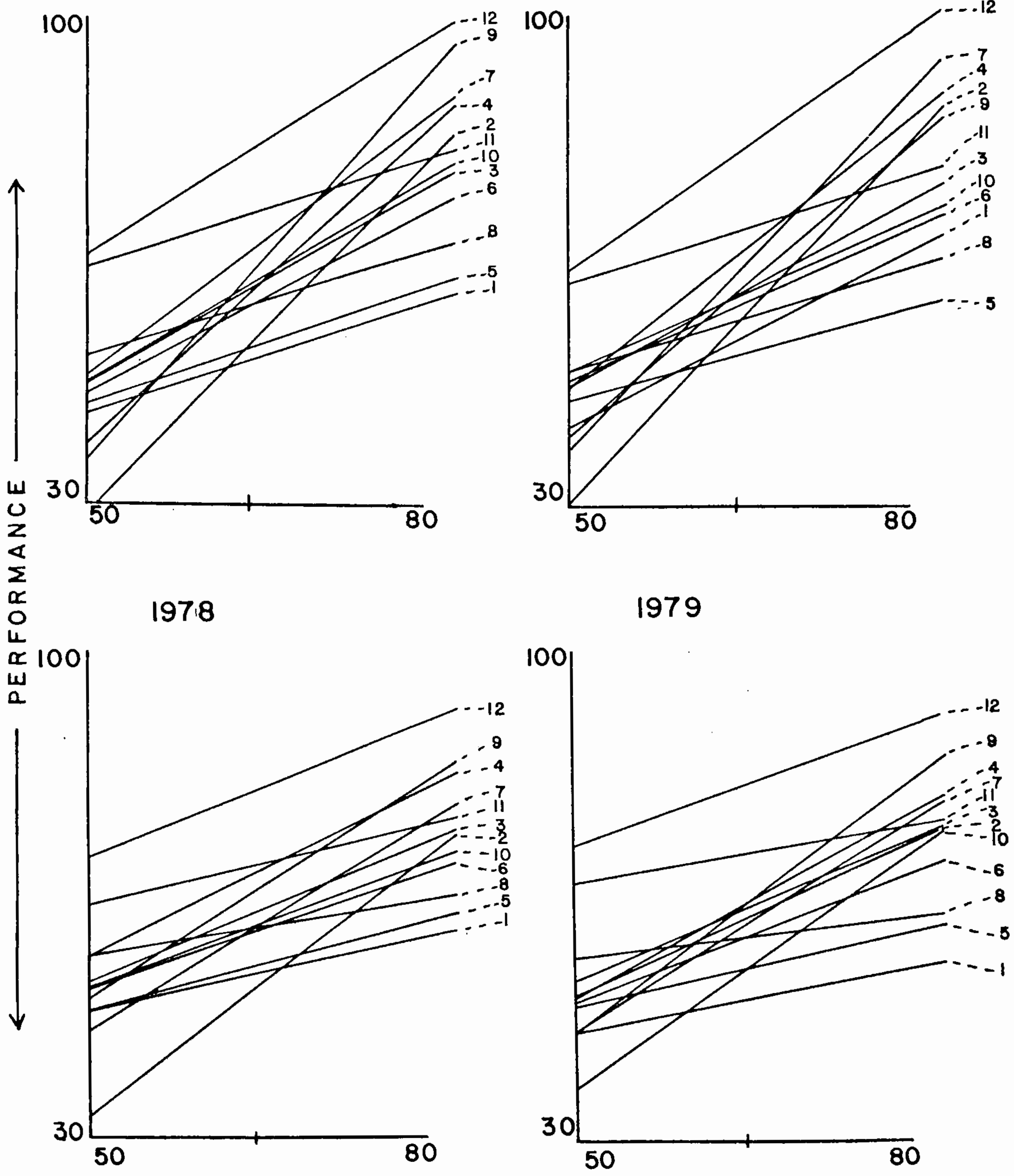
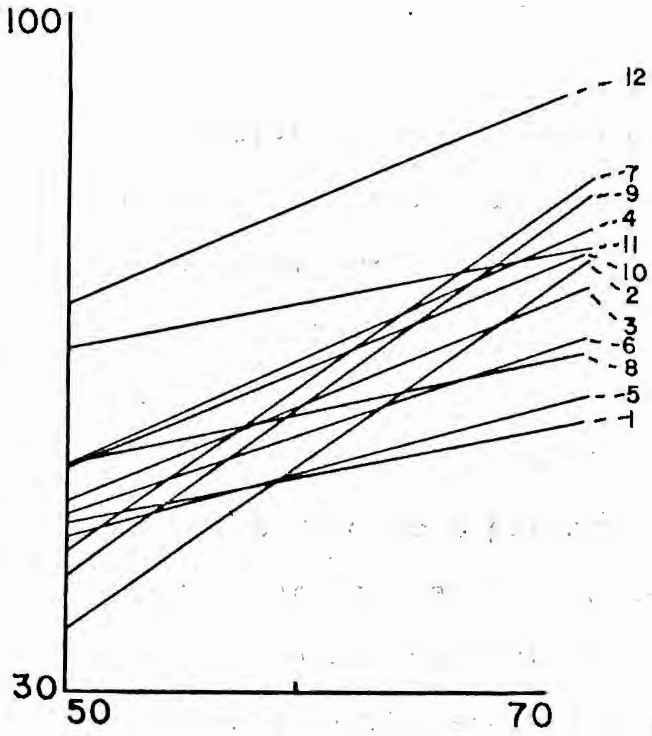
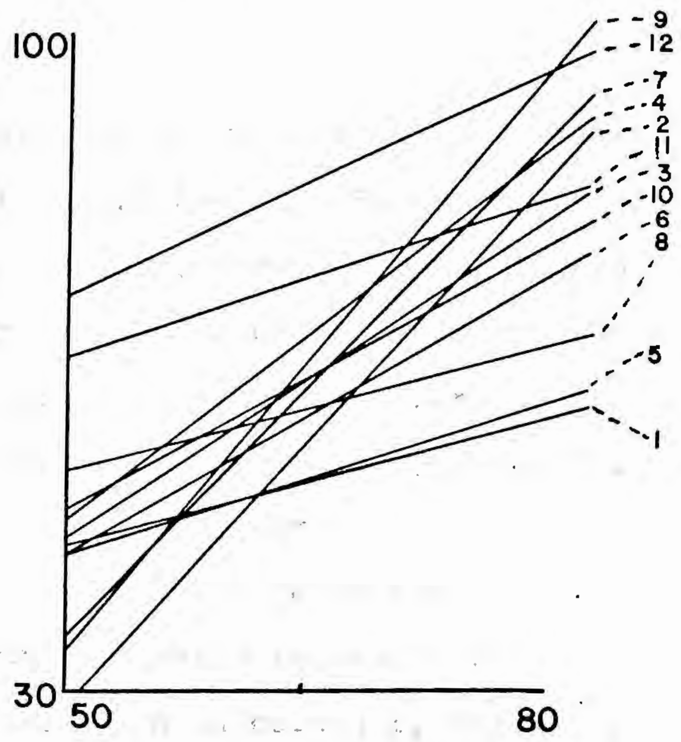
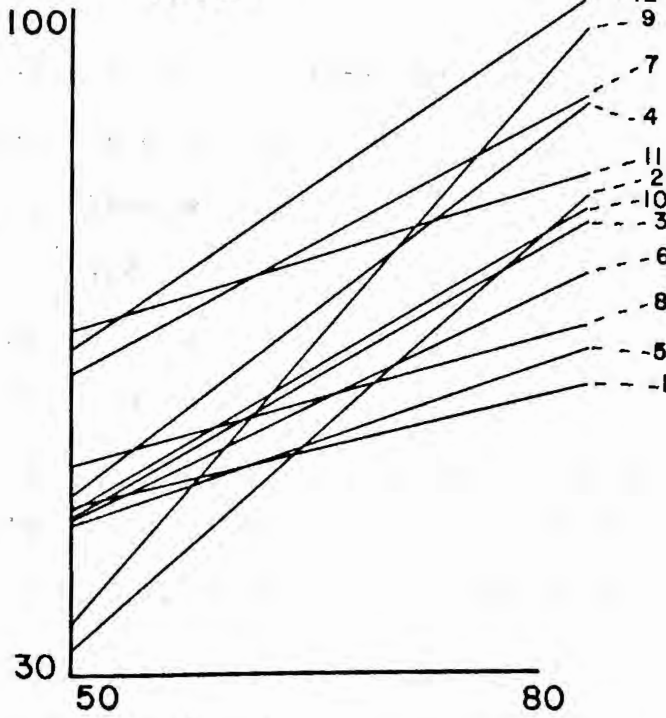


FIG. 1





PERFORMANCE



OBSERVED ENVIRONMENTAL MEAN

FIG. 1

Experiment 2:

Twelve genotypes were evaluated in respect of genotype-environment interaction on coleoptile length. Eight different nutritional germinating mediums were used as the environments in this experiment. Genotypic means over eight environments for twelve genotypes were measured separately in four conjugative years (1977 to 1980) and they are shown in table 12. Different genotypes performed differently for different environments but a close agreement between years was shown by correlation coefficient of mean coleoptile length in four years were highly significant as shown in column 1, table 20. Sonora- 64 showed lowest coleoptile length and the highest coleoptile length was noted in Kazoli.

Analysis of variance of the genotypes were made to test the significant difference of different sources of variation and the results are shown in table 14. All the main items such as genotype (G), environments (E) and the g x e, interaction item were highly significant against the experimental error in all the four years study. When genotype-environment interaction is partitioned, it is clear that the variation can be attributed to differences between the linear regression lines of the twelve genotypes although the remainder of the variation around the regression lines is also significant. The item replication was non-significant in all the four years studied. The mean performance of the genotypes

under varied environments are shown in table 13. Table 13 also shows that the genotypes in general gave better performances in calcium hydroxide [Ca $(OH)_3$] . In others, the performance was poor. The lowest performance was observed in hydrocloric acid [Hcl], in all the years studied. Correlation coefficient between population means in four years study were highly significant (column 2, table 20).

Estimate of the variances δ^2_g, δ^2_e , $\delta^2_{g \times e}$ and δ^2_{ω} are shown in table 15. The influence of $\delta^2_{g \times e}$ was greater than δ^2_g in all the four years study. Genotype x environmental effects suggest importance of the expression of coleoptile length of wheat.

The environmental values ej and the additive genetical components, d_i, obtained separately in each environment in four years study, are shown in tables 16 and 17. The ej values obtained from all the years were more or less similar to each other in a particular environment. Additive genetical components were found to be similar in different years. It was highest in Tanori- 71 and lowest in Kazoli.

Regression techniques for studying the genotype-environment interactions are among the most widely used methods for investigating the response patterns of the genotypes. For each genotype the linear regression (b) of individual value

on the environmental indices (ej) were computed as proposed by Finlay and Wilkinson, (1963). Actual regression lines of performances of the genotypes are shown in figure 2. The genotypic differences were very marked in calcium hydroxide [$Ca(OH)_2$], compared to hydrocloric acid [HCl]. The regression coefficient (b) and the standard errors (S_b) are shown in table 18. The distribution of the values of regression coefficient (b) in four years study of the genotypes were heterogenous, hence all the genotypes have different response is the different environments. Mexipak- 65, Innia- 66, Norteno- 67, Sonalika, Penkty, Janak and Kazoli had an above average response in all the four years study and consistently had high coleoptile length in all above-average environments. Sonora- 64, Tanori- 71, Jupatica- 70, Noori and Dirk, on the other hand, have a response that is below average and had short coleoptile length in below average environments in all the four years studied. Innia- 66 showed highest coleoptile length is good environments and is marked by a high response (b = 2.24, 2.05, 1.96 and 2.34), but Dirk showed a comparatively short coleoptile length (b = 0.25, 0.19, 0.09 and 0.23) in all the environments.

The standard errors proves to be heterogenous as the Chi-square (χ^2) in the Bartlett's test (shown at the bottom of the table 18) was highly significant in all the four different years. Thus it indicated that there were distinct

differences between genotypes around the regression slopes. From the heterogenous S_b values (table 18), Sonora- 64, Tanori- 71 and Dirk were the stable genotypes whereas, Kazoli showed least stability in all the four years studied.

Results obtained from the different independent environmental values (Z_j) as those described in experiment 1 are shown in tables 21 and 22. The joint remainder of table 21 was non significant. The joint regression coefficient was also found not to deviate from one. In table 22 the heterogeneity of regression and the heterogeneity of the remainder were highly significant. These results were found to be very similar in all the four years study. It indicates that for coleoptile length of wheat, or for evaluation of genotypes in respect of genotype x environmental effects, one can use independent environment.

Table 12: Genotypic mean.

Genotypes	1977	1978	1979	1980
1. Sonora- 64	53.17	51.67	54.29	43.76
2. Mexipak- 65	56.09	59.12	57.32	55.95
3. Innia- 66	61.23	64.44	61.29	59.73
4. Norteno- 67	67.05	69.83	64.95	65.55
5. Sonalika	64.11	69.12	63.54	64.09
6. Tanori- 71	52.77	50.23	49.17	52.36
7. Jupatica- 70	57.19	58.76	56.05	54.24
8. Noori	60.22	64.06	60.93	57.00
9. Penkty	64.19	61.95	63.22	63.20
10. Janak	69.32	71.94	73.17	68.59
11. Dirk	71.55	70.22	70.93	67.23
12. Kazoli	78.17	79.00	74.13	78.05

Table 13: Population mean.

	$NaCl_2$ 0.2%	$NaCl_2$ 0.5%	$NaCl_2$ 0.7%	$NaCl_2$ 1%	$Na(OH)_2$	$Ca(OH)_3$	Hcl	control	Mean
1977	52.14	65.04	66.21	67.04	59.94	77.22	47.23	68.55	62.92
1978	57.22	62.65	70.32	67.24	57.36	81.23	49.95	67.55	64.19
1979	48.59	66.14	65.11	66.15	62.11	74.32	51.05	66.06	62.44
1980	53.36	61.04	64.75	65.73	58.05	77.14	47.16	65.95	61.64

Table 14: Results of analysis of variance (m.s.)

Item	d.f.	1977	1978	1979	1980
Nutrition (E)	7	639.74***	648.91***	510.48***	576.70***
Genotype (G)	11	417.32***	498.77***	410.54***	402.87***
G x E	77	96.65***	106.81***	127.71***	130.67***
Regression	11	219.15***	254.14***	205.27***	160.79***
Remainder	66	76.23***	82.25***	114.79***	125.65***
Reps.	3	24.05	29.16	47.23	49.55
Error	285	40.73	27.96	62.21	51.46

*** Significant at 0.1% level.

Table 15: Estimates of variance components.

Components	1977	1978	1979	1980
Genotypes $\delta^2 g$	10.02	12.24	8.38	8.51
Environments $\delta^2 e$	12.47	12.93	9.33	10.94
Genotypes x environments $\delta^2 ge$	13.98	19.71	16.37	19.80
Within Genotypes and environments δ^2_{ω}	40.73	27.96	62.21	51.46

Table 16: Environmental values (ej).

	$Nacl_2$ 0.2%	$Nacl_2$ 0.5%	$Nacl_2$ 0.7%	$Nacl_2$ 1%	$Na(OH)_2$	$Ca(OH)_3$	Hcl	Control
1977	10.78	-2.12	-3.29	-4.14	2.98	-14.30	15.69	-5.63
1978	6.97	1.54	-6.13	-3.05	6.83	-17.04	14.24	-3.36
1979	13.85	-3.70	-2.67	-3.71	0.33	-11.88	11.39	-3.62
1980	8.28	0.60	-3.11	-4.09	3.59	-15.50	14.48	-4.31

Table 17: Additive genetical components, (d_i)

Genotype	1977	1978	1979	1980
1. Sonora- 64	9.75	12.52	8.12	7.88
2. Mexipak- 65	6.83	5.07	5.09	5.69
3. Innia- 66	1.69	-0.25	1.12	1.91
4. Norteno- 67	-4.13	-5.64	-2.54	-3.91
5. Sonalika	-1.19	-4.93	-1.13	-2.45
6. Tanori- 71	10.15	13.96	13.24	9.28
7. Jupatica	5.73	5.43	6.36	7.40
8. Noori	2.70	0.13	1.48	4.64
9. Penkty	-1.27	2.24	-0.81	-1.56
10. Janak	-6.40	-7.75	-10.76	-6.95
11. Dirk	-8.63	-6.03	-8.52	-5.59
12. Kazoli	-15.25	-14.81	-11.72	-16.41

Table 18: Regression co-efficient (b_i) with standard errors, (S_b)

Genotypes	1977		1978		1979		1980	
	b	S_b	b	S_b	b	S_b	b	S_b
1. Sonora- 64	0.41	0.04	0.46	0.14	0.39	0.04	0.42	0.06
2. Mexipak- 65	1.31	0.33	1.26	0.09	1.47	0.39	1.42	0.29
3. Innia- 66	2.24	0.09	2.05	0.49	1.96	0.27	2.34	0.61
4. Norteno- 67	1.56	0.51	1.46	0.36	1.79	0.10	1.43	0.41
5. Sonalika	1.24	0.24	1.32	0.14	1.05	0.07	1.15	0.19
6. Tanori- 71	0.13	0.03	0.32	0.04	0.26	0.04	0.14	0.07
7. Jupatica- 70	0.44	0.15	0.49	0.11	0.36	0.11	0.44	0.14
8. Noori	0.83	0.19	0.95	0.23	0.91	0.27	0.80	0.12
9. Penkty	1.05	0.29	1.14	0.15	1.09	0.19	0.96	0.21
10. Janak	1.03	0.16	1.04	0.24	1.32	0.32	1.16	0.27
11. Dirk	0.25	0.07	0.19	0.03	0.09	0.16	0.23	0.07
12. Kazoli	1.51	0.64	1.32	0.27	1.31	0.25	1.54	0.37
χ^2 = (d.f. 11)	101.98***		76.99***		66.36***		73.12***	

*** Significant at 0.1% level.

Table 19: Linear interaction co-efficients, (β_i)

Genotypes	1977	1978	1979	1980
1. Sonora- 64	-0.59	-0.54	-0.61	-0.58
2. Mexipak- 65	0.31	0.26	0.47	0.42
3. Innia- 66	1.24	1.05	0.96	1.34
4. Norteno- 67	0.56	0.46	0.79	0.43
5. Sonalika	0.24	0.32	0.05	0.15
6. Tanori- 71	-0.87	-0.68	-0.74	-0.86
7. Jupatica- 70	-0.56	-0.51	-0.64	-0.56
8. Noori	-0.17	-0.05	-0.09	-0.20
9. Penkty	0.05	0.14	0.09	-0.04
10. Janak	0.03	0.04	0.32	0.16
11. Dirk	-0.75	-0.81	-0.91	-0.77
12. Kazoli	0.51	0.32	0.31	0.54

Table 20: Correlation studies.

	Between Genotypic mean	Between Population mean	Between Regression coefficients
1977 vs. 1978	0.9529	0.9483	0.9877
79	0.9603	0.9645	0.9556
80	0.9809	0.9859	0.9987
1978 vs. 1979	0.9467	0.8645	0.9590
80	0.8358	0.9799	0.9745
1979 vs. 1980	0.9398	0.9248	0.9507

Table 21: Testing the adequacy of the independent environmental assessors $(a)_i$, $(a)_{ii}$, $(b)_i$ and $(b)_{ii}$ from the significance of joint regression, $\bar{\beta}$ from one and of the joint remainder.

Item	d.f.	$(a)_i$	$(a)_{ii}$	d.f.	$(b)_i$	$(b)_{ii}$
			1977			
$\bar{\beta}$		0.97	0.99		0.96	1.02
$\bar{\beta}$ -1		-0.03	-0.01		-0.04	0.02
Joint Remainder	6	21.54	30.32	6	16.92	27.11
Error	285	46.73	31.44	141	41.13	47.69
			1978			
$\bar{\beta}$		0.94	1.04		0.95	0.97
$\bar{\beta}$ -1		-0.06	0.04		-0.05	-0.03
Joint Remainder	6	6.95	16.02	6	17.14	9.93
Error	285	21.24	27.62	141	24.33	20.76
			1979			
$\bar{\beta}$		0.96	0.99		0.93	0.99
$\bar{\beta}$ -1		-0.04	-0.01		-0.07	-0.01
Joint Remainder	6	42.23	40.67	6	14.46	42.93
Error	285	66.33	61.19	141	60.55	69.13
			1980			
$\bar{\beta}$		1.02	1.06		0.98	0.94
$\bar{\beta}$ -1		0.02	0.06		-0.02	-0.06
Joint Remainder	6	33.21	30.66	6	21.43	40.69
Error	285	42.19	47.32	141	42.20	41.67

Table 22: Significance of heterogeneity of remainder using the environmental assessors $(a)_i$, $(a)_{ii}$, $(b)_i$ and $(b)_{ii}$.

Item	d.f.	$(a)_i$	$(a)_{ii}$	d.f.	$(b)_i$	$(b)_{ii}$
			1977			
Heterogeneity of Regression	11	247.62***	197.77***	5	361.62***	287.55***
Heterogeneity of Remainder	66	81.94***	95.32***	30	112.93***	149.66***
Error	285	46.73	31.44	141	41.13	47.69
			1978			
Heterogeneity of Regression	11	187.32***	224.66***	5	214.73***	189.33***
Heterogeneity of Remainder	66	79.64***	114.92***	30	106.93***	164.65***
Error	285	21.24	27.62	141	24.33	20.76
			1979			
Heterogeneity of Regression	11	236.21**	204.53**	5	288.22***	369.64***
Heterogeneity of Remainder	66	114.69***	176.32***	30	194.06***	214.05***
Error	285	66.33	61.19	141	60.55	69.13
			1980			
Heterogenity of Regression	11	304.66***	280.19***	5	309.06***	319.32***
Heterogeneity of Remainder	66	194.22***	176.66***	30	144.00***	204.66***
Error	285	42.19	47.32	141	42.20	41.67

,* Significant at 1% and 0.1% level respectively.

Fig. 2: Phenotypic regression of coleoptile length for different genotypes against environment (nutrition) means.

1. Sonora- 64
2. Mexipak- 65
3. Innia- 66
4. Norteno- 67
5. Sonalika
6. Tanori- 71
7. Jupatica- 70
8. Noori
9. Penkty
10. Janak
11. Dirk
12. Kazoli

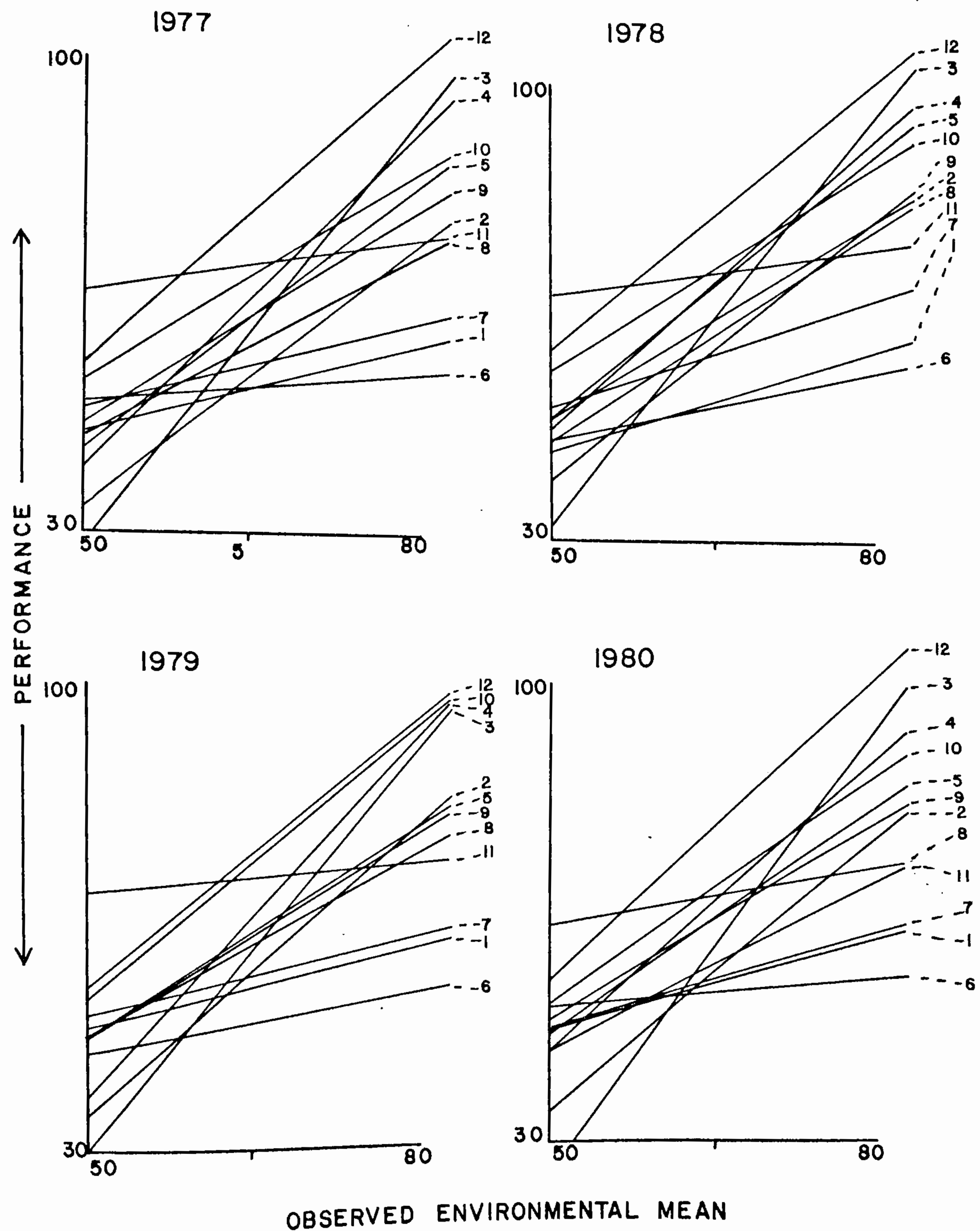


FIG. 2

Experiment 3:

Genotypic means over sixteen different combinations of N,P,K and Ca environments for twelve genotypes were evaluated in respect of genotype-environment interaction as shown by coleoptile length. The genotypes were measured separately in each year and they are shown in table 23. Genotypic means varied within twelve genotypes but a close agreement between years was shown by correlation coefficient of mean coleoptile length in four years (1978 to 1981). These were highly significant, as shown in column 1, table 31. Low and high genotypic means performance in all the four years were found in Sonora- 64 and Kazoli respectively.

Results of analysis of variance in all the four years study are shown in table 25. Analysis of variance of the data showed that the mean differences between the genotypes (G) and between environments (E) were highly significant. The genotype x environment interaction was also highly significant; when this interaction is partitioned, it is clear that most of the variations can be attributed to differences between the linear regression lines of the genotypes although the remainder of the variation around the regression lines is also significant. Means of the twelve genotypes over sixteen different environments in all the four years study are shown in table 24. The table shows that the genotypes were affected by different environments. The environmental means (table 24) also show that

genotypes in general gave better performances in P, K, and Ca combination environments. Highest coleoptile length was obtained in PKCa whereas, the lowest was obtained in PCa. A close agreement in the result obtained in four years as the correlation coefficient were highly significant (column 2, table 31).

The estimates of $\delta^2 g$, $\delta^2 e$, $\delta^2 gxe$ and δ^2_w as derived from the analysis of variance of the twelve genotypes over sixteen environments are given in table 26. The influence of $\delta^2 e$ and $\delta^2 gxe$ was greater than $\delta^2 g$ in all the four years study suggesting importance of genotype-environment interaction in coleoptile length of wheat.

Estimates of the additive environmental values ej which were used in the phenotypic regression analysis were obtained and are shown in table 27. The ej values obtained from all the years were more or less similar to each other in a particular environment. It was highest in NPK and lowest in PKCa. Additive genetical components, (d_i) in four different years are shown in table 28. These genetical components were found to be similar and it was highest in Sonora- 64 and lowest in Kazoli.

Regression techniques for studying the genotype-environment interactions are among the most widely used methods for investigating the response patterns of the genotypes. For each genotype the linear regression (b_i) of individual values

on the environmental means were computed and they are shown in table 29. The linear regression coefficients in table 29 correspond to the b_i values of Finlay and Wilkinson (1963); and for convenience of comparison of regression values, the β_i values are shown in table 30. Actual regression lines of performance of each genotype against the corresponding environmental means are shown in figure 3. A clear indication of genotype x environment interaction effects was reflected in the figure. The genotypic differences were very marked in NPK compared to PKCa environments on coleoptile length in all the four different years studied.

The regression coefficients (b_i), standard error (S_b) are shown in table 29. As revealed by joint regression, the distribution of all the genotypes b_i values were heterogenous and for this all the genotypes had different response to different environments. Mexipak- 65, Innia-66, Jupatica- 70, Penkty and Kazoli had an above average response in all the four different years and had a consistently high coleoptile length in all above-average environments. Sonora- 64, Norteno-67, Sonalika, Noori, Janak and Dirk, On the other hand, have a response below the average and showed short coleoptile length in below average environments in all the four years studied. Jupatica- 70 showed highest coleoptile length in good environments as marked by a high response (b = 2.06, 1.84, 1.76, and 1.83), but Dirk showed a comparative short coleoptile length

(b = 0.31, 0.46, 0.39 and 0.37) in poor environments. The S_b values were found to be heterogenous as the χ^2 was highly significant (χ^2 = 101.98, 76.99, 66.36 and 73.12) in all the four years study and indicated that there were distinct differences between genotypes around the regression slopes. Among the twelve genotypes Dirk showed most stable genotype as shown by their low S_b values whereas, Jupatica- 70 showed least stability as shown by their high S_b values.

Different independent environmental values (Z_j), as those described in experiment 1, are shown in table 32 and 33. The joint remainder (table 32) was non significant and the joint regression coefficient $\bar{\beta}$, should not deviate from one in all the four different years. In table 33 the heterogeneity of regression and the heterogeneity of remainders were highly significant in all the four years. These results indicate that for coleoptile length of wheat or for evaluation of genotypes in respect of genotype-environmental effects one can use independent environment.

Table 23: Genotypic mean.

Genotypes	1978	1979	1980	1981
1. Sonora- 64	49.23	54.16	51.59	53.75
2. Mexipak- 65	57.73	58.29	53.29	56.27
3. Innia- 66	64.73	60.19	64.05	62.32
4. Norteno- 67	67.55	64.19	69.23	67.05
5. Sonalika	52.32	54.76	59.23	50.75
6. Tanori- 71	60.23	61.05	57.62	59.15
7. Jupatica- 70	64.76	64.03	62.19	60.54
8. Moori	54.76	58.23	59.76	58.10
9. Penkty	60.23	66.05	64.59	65.73
10. Janak	62.19	60.73	60.55	62.93
11. Dirk	70.73	69.82	73.94	71.59
12. Kazoli	82.32	79.76	78.93	79.05

Table 24: Population mean.

Environment	1978	1979	1980	1981
N	56.34	58.83	53.66	54.22
P	61.15	59.12	63.32	60.06
K	71.31	64.23	72.05	73.10
Ca	68.26	75.17	75.23	68.05
NP	53.64	51.05	52.18	57.24
NK	61.69	62.62	60.19	59.39
NCa	60.96	59.23	62.93	63.11
PK	61.02	64.69	65.23	65.15
PCa	52.05	53.22	54.17	50.73
KCa	58.18	61.70	60.22	62.17
NPK	51.42	54.30	49.74	51.69
NPCa	53.79	54.73	52.05	53.20
NKCa	74.24	72.65	69.73	72.33
PKCa	77.65	75.73	79.96	76.90
NPKCa	67.19	66.30	70.79	65.19
Control	67.07	69.11	65.12	64.73

Table 25: Results of analysis of variance (m.s.)

Item	d.f.	1978	1979	1980	1981
Nutrition (E)	15	969.98***	884.23***	1228.17***	920.12***
Genotype (G)	11	1183.73***	743.38***	955.34***	920.36***
GxE	165	196.05***	242.28***	217.64***	377.31***
Regression	11	476.05***	623.55***	506.66***	932.67***
Remainder	154	176.05***	215.05***	197.00***	337.64***
Replication	3	84.05	91.14	93.79	64.55
Error	573	162.35	88.76	97.64	105.18

***Significant at 0.1% level.

Table 26: Estimates of variance components.

Item	1978	1979	1980	1981
Genotype $\delta^2 g$	15.43	7.82	11.52	8.48
Environments $\delta^2 e$	16.82	16.57	23.55	16.97
Genotypes x Environments $\delta^2 gxe$	8.42	38.38	30.00	68.03
Within genotypes and environments $\delta^2 w$	162.35	88.76	97.64	105.18

Table 27: Environmental values (ej).

Environment	1978	1979	1980	1981
N	5.91	3.83	9.25	8.10
P	1.10	3.54	-0.41	1.76
K	-9.06	-1.57	-9.14	-10.78
Ca	-6.01	-12.51	-12.32	-5.73
NP	8.61	11.61	10.73	5.08
NK	0.56	0.04	2.72	2.93
NCa	1.29	3.43	-0.02	-0.79
PK	1.23	-2.03	-2.32	-2.83
PCa	10.20	9.44	8.74	11.59
KCa	4.07	0.96	2.69	0.15
NPK	10.83	8.36	13.17	10.63
PCa	8.46	7.93	10.86	9.12
NKCa	-11.99	-9.99	-6.82	-10.01
PKCa	-15.40	-13.07	-17.05	-14.58
NPKCa	-4.94	-3.64	-7.88	-2.87
Control	-4.82	-6.45	-2.21	-2.41

Table 28: Additive genitical components, (d_i)

Genotypes	1978	1979	1980	1981
1. Sonora- 64	13.00	8.45	11.32	8.51
2. Mexipak- 65	4.50	4.32	9.62	6.00
3. Innia- 66	-2.50	2.42	-1.14	-0.05
4. Norteno- 67	5.32	-1.58	-6.32	-4.78
5. Sonalika	9.91	7.85	3.68	11.52
6. Tanori- 71	2.00	1.56	5.29	3.12
7. Jupatica	2.53	-1.42	0.72	1.73
8. Noori	7.47	4.38	3.15	4.17
9. Penkty	2.00	-3.44	-1.68	-3.46
10. Janak	0.04	1.88	2.36	-0.66
11. Dirk	-8.50	-7.21	-10.43	-0.32
12. Kazoli	-20.09	-17.15	-16.02	-16.78

Table 29: Regression co-efficients (b) with standard errors (S_b).

Genotypes	1978		1979		1980		1981	
	b	S_b	b	S_b	b	S_b	b	S_b
1. Sonora- 64	0.64	0.19	0.47	0.22	0.53	0.16	0.59	0.14
2. Mexipak- 65	1.95	0.32	1.67	0.31	1.75	0.44	1.83	0.73
3. Innia- 66	0.94	0.15	1.05	0.19	0.96	0.22	1.15	0.05
4. Norteno- 67	0.75	0.41	0.96	0.31	1.03	0.12	0.69	0.20
5. Sonalika	0.49	0.21	0.64	0.11	0.53	0.16	0.47	0.09
6. Tanori- 71	1.05	0.26	1.12	0.11	0.98	0.21	0.94	0.22
7. Jupatica- 70	2.06	0.44	1.84	0.49	1.76	0.45	1.83	0.61
8. Noori	0.44	0.17	0.47	0.22	0.31	0.19	0.54	0.17
9. Penkty	1.79	0.63	1.49	0.22	1.66	0.39	1.83	0.44
10. Janak	0.76	0.22	0.73	0.16	0.84	0.14	0.69	0.31
11. Dirk	0.31	0.04	0.46	0.20	0.39	0.11	0.37	0.04
12. Kazoli	0.82	0.21	1.10	0.14	1.26	0.24	1.07	0.16
χ^2 = (d.f. 11)	113.91***		66.75***		80.00***		212.87***	

***Significant at 0.1% level.

Table 30: Linear interaction co-efficient, (β_i).

Genotypes	1978	1979	1980	1981
1. Sonora- 64	-0.36	-0.53	-0.47	-0.41
2. Mexipak- 65	0.95	0.67	0.75	0.83
3. Innia- 66	-0.06	0.05	-0.04	0.15
4. Norteno- 67	-0.25	-0.04	0.03	-0.31
5. Sonalika	-0.51	-0.36	-0.47	-0.53
6. Tanori- 71	0.05	0.12	-0.02	-0.06
7. Jupatica- 70	1.06	0.84	0.76	0.83
8. Noori	-0.56	-0.53	-0.69	-0.46
9. Penkty	0.79	0.49	0.66	0.83
10. Janak	-0.24	-0.27	-0.16	-0.31
11. Dirk	-0.69	-0.54	-0.61	-0.63
12. Kazoli	-0.18	0.10	0.26	0.07

Table 31: Correlation studies

	Between geno-typic mean	Between popu-lation mean	Between regression co-efficients
1978 vs. 1979	0.9418	0.9129	0.9597
80	0.9679	0.9442	0.9431
81	0.9395	0.9577	0.9747
1979 vs. 1980	0.9043	0.9091	0.9748
81	0.9584	0.8613	0.9566
1980 vs. 1981	0.9203	0.9385	0.9522

Table 32: Testing the adequacy of the independent environmental assessors $(a)_i$, $(a)_{ii}$, $(b)_i$ and $(b)_{ii}$ from the significance of joint regression $\bar{\beta}$, from one and of the joint remainder.

Item	d.f.	$(a)_i$	$(a)_{ii}$	d.f.	$(b)_i$	$(b)_{ii}$
			1978			
$\bar{\beta}$		1.04	0.99		0.91	0.94
$\bar{\beta}-1$		0.04	-0.01		-0.09	-0.06
Joint Remainder	14	81.82	116.93	14	139.33	109.70
Error	573	171.19	176.62	285	160.21	165.73
			1979			
$\bar{\beta}$		0.97	0.98		0.94	0.96
$\bar{\beta}-1$		-0.03	-0.02		-0.06	-0.04
Joint Remainder	14	91.55	62.32	14	81.15	29.66
Error	573	104.03	114.33	285	96.92	94.73
			1980			
$\bar{\beta}$		1.03	0.95		1.06	1.02
$\bar{\beta}-1$		0.03	-0.05		0.06	0.02
Joint Remainder	14	26.55	35.39	14	81.03	64.55
Error	573	89.67	91.36	285	94.22	90.70
			1981			
$\bar{\beta}$		0.99	0.96		0.89	0.94
$\bar{\beta}-1$		-0.01	-0.04		-0.11	-0.06
Joint Remainder	14	61.39	62.84	14	14.73	60.55
Error	573	94.81	101.94	285	90.39	92.67

Table 33: Significance of heterogeneity of remainder using the environmental assossors $(a)_i$, $(a)_{ii}$, $(b)_i$ and $(b)_{ii}$.

Item	d.f.	$(a)_i$	$(a)_{ii}$	d.f.	$(b)_i$	$(b)_{ii}$
			1978			
Heterogeneity of Regression	11	621.03***	409.66***	5	569.03**	622.55**
Heterogeneity of Remainder	154	436.73***	193.73***	70	297.62***	317.05***
Error	573	171.19	176.62	285	160.21	165.73
			1979			
Heterogeneity of Regression	11	496.75***	553.55***	5	411.60***	497.60***
Heterogeneity of Remainder	154	321.70***	330.46***	70	293.36***	304.19***
Error	573	104.03	114.33	285	96.92	94.73
			1980			
Heterogeneity of Regression	11	397.29***	412.50***	5	411.49***	403.45***
Heterogeneity of Remainder	154	204.66***	226.63***	70	197.69***	216.66***
Error	573	89.67	91.36	285	94.22	90.70
			1981			
Heterogeneity of Regression	11	397.65***	401.75***	5	407.09***	318.95***
Heterogeneity of Remainder	154	196.05***	209.93***	70	216.04***	200.55***
Error	573	94.81	101.94	285	90.39	92.67

**, *** Significant at 1% and 0.1% level respectively.

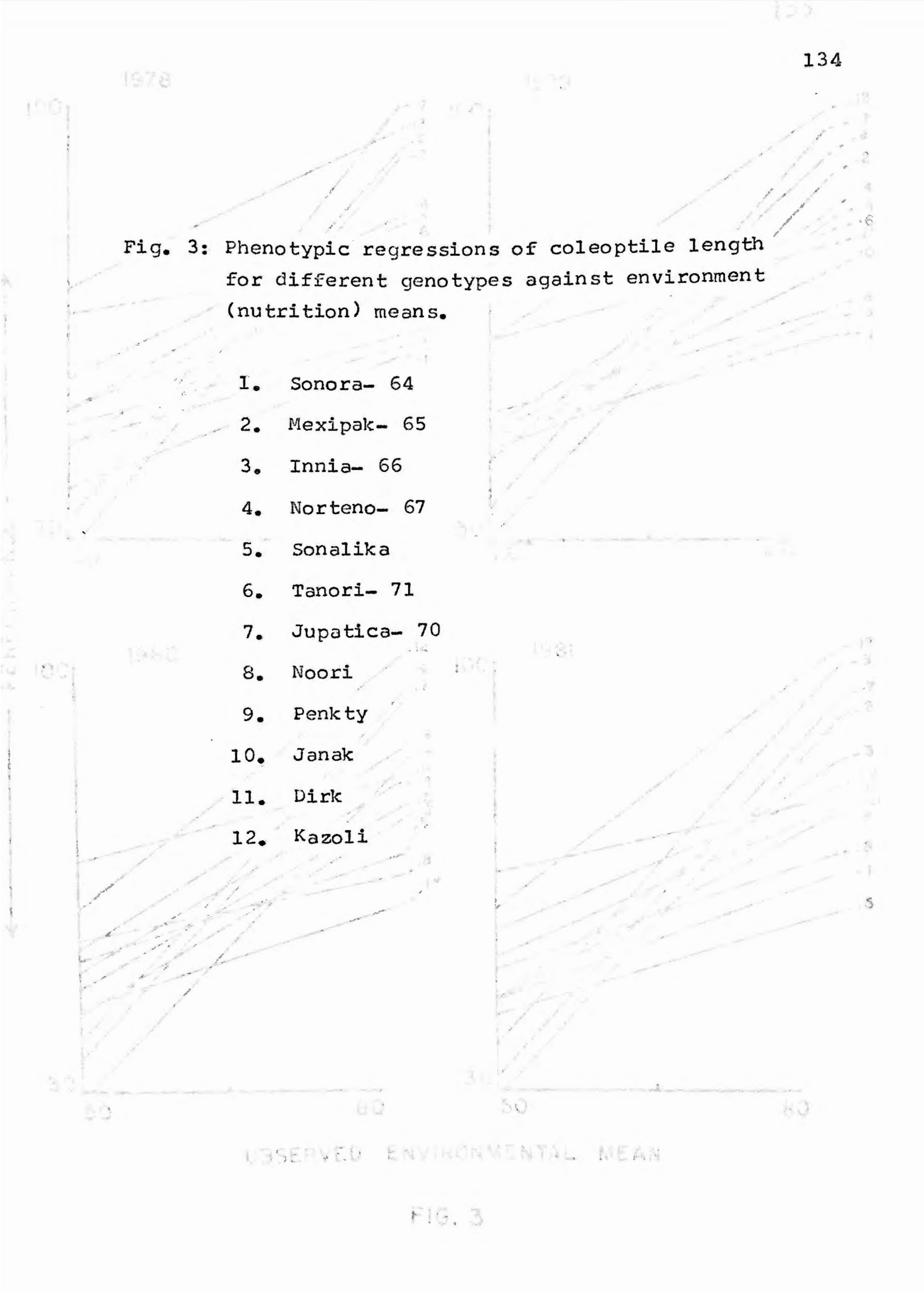


Fig. 3: Phenotypic regressions of coleoptile length for different genotypes against environment (nutrition) means.

1. Sonora- 64
2. Mexipak- 65
3. Innia- 66
4. Norteno- 67
5. Sonalika
6. Tanori- 71
7. Jupatica- 70
8. Noori
9. Penkty
10. Janak
11. Dirk
12. Kazoli

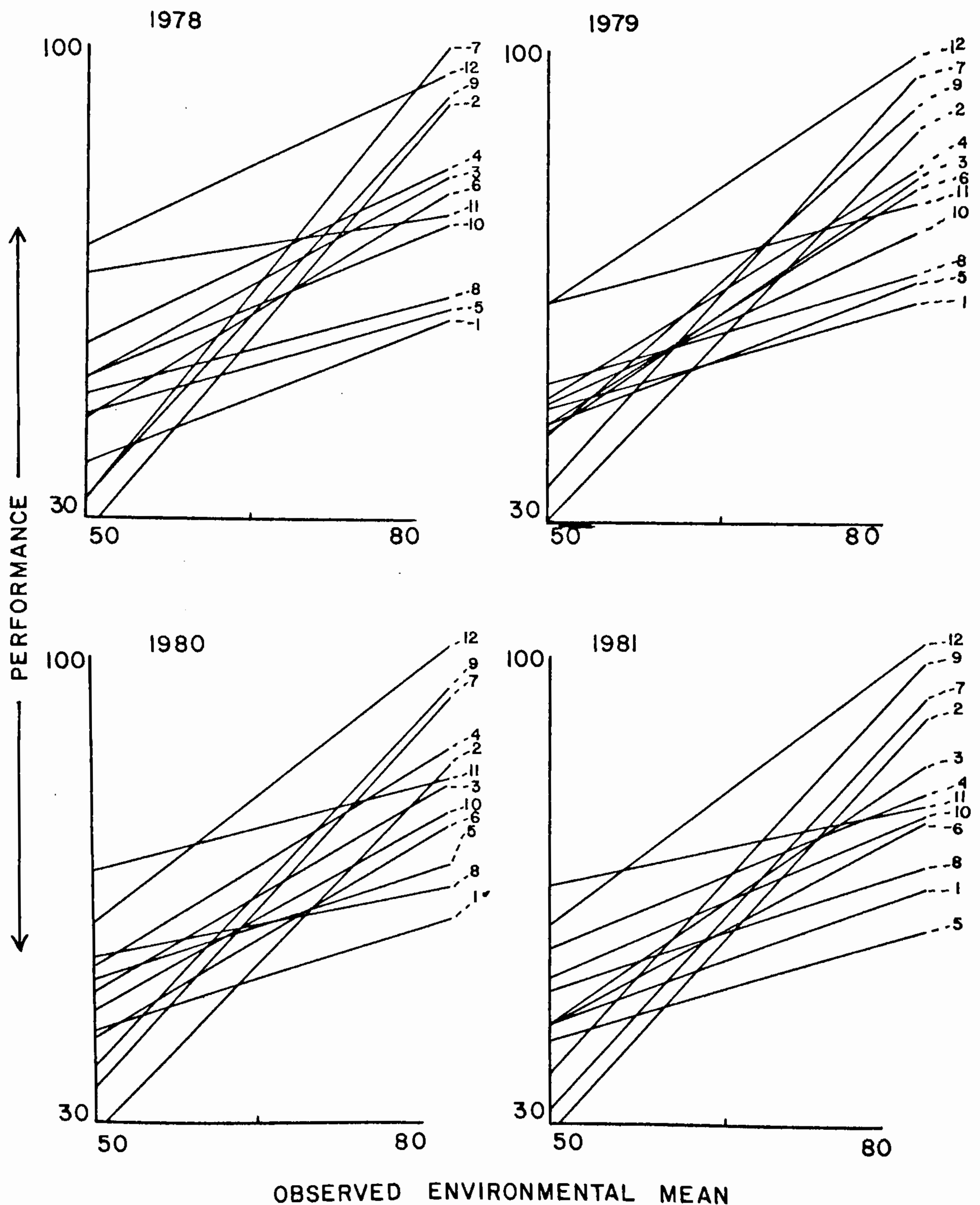


FIG. 3

Experiment 4:

The materials used in this experiment consisted of two parental genotypes, their F_1 and 60 inbred lines (F_7 and F_8) were assessed in respect of genotype-environmental interaction shown by coleoptile length grown under sixteen different combinations of the presence and absence of N,P,K and Ca germinating medium under which seedling raised were treated as environments. The mean of the two parental genotypes and their F_1 over sixteen different environments are shown in table 34. This experiment was repeated in two years (1981 and 1982). The mean, m, and the additive, [d], and the dominance, [h], (table 34) genetical components have been estimated from the average performance over environments of the two parental genotypes (P_1 = Mexipak- 65 and P_2 = Janak) and their F_1 over all environments assuming that this simple model is adequate. From the sign of [d] the table shows that Janak had highest coleoptile length than Mexipak- 65 in all the years studied. There is a directional component of dominance [h] for highest coleoptile length in the years 1979 and 1982 but a significant directional component was not found for the years 1980 and 1981.

The results of analysis of variance are shown in table 36. In the analysis of variance most of the items were significant against the experimental error in both the years. The item parents and F_1, (P) was significant in the year 1981 and highly

significant in the year 1982. The main item genotype (G) was highly significant in both the two years studied, indicating that there is real difference among the genotypes. A real effect of environments was also noted as the main item (E) was highly significant. Genotype-environmental interaction, (GxE) effects were significant in both parents and F_1 and the inbred lines.

The mean of the two parental genotypes and of their 60 inbred lines over environments are given in table 35 along with the difference between their two means, the standard deviation of the difference and the significance of the difference from zero. The difference is non-significant for all the two years studied. Signs of difference in the year 1981 is negative since, on average, the inbred lines had higher coleoptile length than the parents.

The estimates of the variance for genotypes, $\delta^2 g$, environments, δ^2_e, genotype x environments, δ^2_{gxe}, and within genotypes and environments (between individuals), δ^2_w, as derived from an analysis of variance (table 36) of the parents and F_1 and their 60 inbred lines over environments are given in table 37. The two main effects and their interaction are highly significant in the years 1981 and 1982. The genotype-environmental interaction component of variation δ^2_{gxe}, is however, consistently high in two years suggesting importance of genotype-

environmental interaction effects in the expression of coleoptile length.

The genotype-environmental interactions of the 60 inbred lines were investigated for linearity by regressing their performance in each environment against a biological measure of the environments. For comparative purposes, four kinds of material were used to assess these environments. They are given in descending order of relationship of the 60 inbred lines whose interactions were investigated.

(a) Dependent ej.

The performance of each of the 60 inbred lines was regressed against the mean of all 60 lines in each environment, i.e. the material used for the environmental assessment is the same as that which was to be investigated.

(b) Independent Z_j using replicate individuals.

Each inbred line in each environment was represented by ten individual seedlings. These were split at random into two groups of five, the interactions of one group were to be investigated and the other group was to contribute to the environmental assessment.

(c) Independent Z_j using replicate sets of inbred lines.

The 60 inbred lines were divided at random into two sets of 30, the interactions of one set were to be investigated and

the other set was to help assess the environment.

(d) Independent Z_j using parental genotypes.

The 60 inbred lines were regressed against the average of the two parental genotypes, Mexipak- 65 and Janak, in each environment from whose F_2 they were derived by selfing.

Groups (b) and (c) were further divided into subgroups $(b)_i$ and $(b)_{ii}$ and $(c)_i$ and $(c)_{ii}$. Subgroups $(b)_i$ and $(b)_{ii}$ represent the regression of the 60 inbred lines in one set of replicate individuals against the mean of the other set in each environment and then vice versa. Similarly, subgroups $(c)_i$ and $(c)_{ii}$ represent the regression of the 30 inbred lines in one set against the mean of the other set in each environment and then vice versa.

The adequacy with which the environments are assessed depends upon the degree of relationship between the genotypes whose interactions are to be investigated and the genotypes used to assess the environment and also upon the purposes for which the genotype-environmental interaction assessments are required. The genotypes are required according to the magnitude of their linear regression coefficients, $\bar{\beta} + \beta_d$ (when derived from the regression of a genotypic performance in each environment against an environmental assessment), the joint regression item to be significant when tested against the joint

remainder. The joint remainder should be non-significant when tested against the variance within genotypes and environments (between individuals) and the joint regression coefficient, $\bar{\beta}$, should not be significantly different from one. In table 38 the results of applying these two criteria to the joint regression analysis of the inbred lines against the three kinds of independent environmental assessors, (b), (c) and (d), are given. The table shows that independent assessment of the environment in the year 1981 and 1982 which consistently satisfies both criteria is a replicate set of individuals, $(b)_i$ and $(b)_{ii}$. A replicate set of inbred lines, $(c)_i$ and $(c)_{ii}$, is satisfactory to the extent that the joint regression coefficient $\bar{\beta}$, is never significantly different from one in both the two years.

In column $(d)_i$ the results of applying the two criteria to the joint regression against the independent environmental assessor (as in $(b)_i$ and $(b)_{ii}$ and $(c)_i$ and $(c)_{ii}$) are given. According to these results, the use of the parental genotypes Mexipak- 65 and Janak to assess the environment consistently fails on both tests. However, the average of the parental genotypes is based upon fewer observations than the average of the 60 inbred lines in each environment. In this case, therefore, unlike (b) and (c), the material used as the independent variate in assessing the environment is subject to a greater sampling variance than the inbred lines used as the dependent variate in the joint regression. In column $(d)_{ii}$

the average, in each environment, of the parents has been regressed against the average, in each environment, of the 60 inbred lines. It is clear that the number of significant tests have been reduced to zero and the joint regression, $\bar{\beta}$, is never significantly different from one in both the two years.

In table 39 the significance of the heterogeneity of regressions and of the heterogeneity of remainders in the joint regression analysis of the parents and inbred lines against the three different kinds of environmental assessors, (b), (c) and (d), are given for each year. The heterogeneity of remainders was tested against the variance within genotypes and environments (between individuals). The heterogeneity of regression was also tested against the variance within genotypes and environments. The results are completely consistent across all the different ways of assessing the environment. Thus for both parents and inbreds there are significant linear and non-linear interactions in both the two years.

The rank correlation (Spearman, 1904) over the 60 inbred lines between the linear regression coefficient, $1 + \bar{\beta}_d$, obtained with the dependent environmental component, e_j, and the corresponding coefficient, $\bar{\beta} + \beta_d$, obtained with each kind of independent environmental component, z_j, are given in table 40. On the basis of these correlations there is

little to choose between the different kinds of environmental assessment since all are highly significant ($P < 0.001$).

Rank correlations over the 60 inbred lines for 58 degrees of freedom between the average variance within environments, δ^2_W , (table 37) and the linear regression coefficient, $\bar{\beta}_d$, and the total variance over environments, $\bar{V}_{G+E}$, which are, respectively, a measure of sensitivity to environmental variation, of linear sensitivity to environmental differences and of total sensitivity (linear and non-linear) are given in table 41. The rank correlation between the linear regression coefficient, $\bar{\beta}_d$, and the variance within genotypes and environments, δ^2_W's is significantly negative, i.e. the linear sensitivity to environmental differences is greater. In the year 1981 there is a positive and in the year 1982 a negative non-significant correlation between the rankings of the total variance over environments, $\bar{V}_{G+E}$, and the average variance within environments, δ^2_W . Hence, there is a fair degree of independence in the genetical control of sensitivity at the environmental levels.

Estimates of the number of effective factors controlling the differences among the lines for the additive genetical component and for the linear regression coefficient (Parkins and Jinks, 1968a; Mather and Jinks, 1971; Eaves and Brumpton, 1972) are given in table 42. The estimate for the additive genetic component $[d]$ are almost the same in the two years

studied. But the estimate for the linear sensitivity β_d showed considerable difference in the year 1981 and 1982. It is equally clear from the absence of significant correlations there are few, if any, effective factors acting in common upon both relative mean performance [d] and linear sensitivity to environmental differences (β_d).

Table 34: The mean, m, and additive, [d], and dominance, [h], genetical components.

	1979	1980	1981	1982
Mean				
P_1	54.36	57.73	51.16	55.32
P_2	71.64	68.73	70.05	76.95
F_1	60.34	64.98	61.11	59.32
Components				
m	63.00*	63.23*	60.60*	66.13*
d	8.64*	5.50*	9.44*	10.81*
h	2.66*	-1.75 n.s.	-0.51 n.s.	6.81*

n.s. Estimate non-significant.

*Significant at 5% level.

Table 35: The parental mean, $\bar{P}$, and the mean of the 60 inbred lines, $\bar{L}$, when averaged over the sixteen environmental treatments.

Item	1981	1982
$\bar{P}$	60.60	66.13
$\bar{L}$	63.15	61.94
Difference	-2.55	4.19
Standard deviation of the difference	4.76	6.21
Probability	n.s.	n.s.

Standard deviation for 990 degrees of freedom

n.s. = Probability is non-significant.

Table 36: Results of analysis of variance (m.s.)

Item	d.f.	1981	1982
Reps.	3	195.32	164.74
Environment (E)	15	1034.44***	1421.92***
Genotype (G)	62	1104.72***	1282.48***
Parents and F_1(P)	2	892.32**	1432.76***
Inbred (I)	59	1126.04***	1295.32***
Remainder (R)	1	271.65	224.88
GxE	930	514.49***	621.34***
PxE	30	497.64***	721.64***
IxE	885	520.44***	624.83***
RxE	15	197.73	214.66
Error	3021	251.72	201.76

,* Significant at 1% and 0.1% level respectively.

Table 37: Estimates of δ^2's of the inbred, parents and F_1.

Components	Parents & F_1		Inbred	
	1981	1982	1981	1982
Genotypes, $\delta^2 g$	11.18	14.59	10.71	16.61
Environments, $\delta^2 e$	6.17	11.11	9.46	10.47
Genotypes x environments, δ^2_{ge}	61.48	127.97	67.18	105.77
Within genotype and environments, δ^2_w	251.72	201.76	251.72	201.76

Table 38: Testing the adequacy of the independent environmental assessors $(b)_i$, $(b)_{ii}$, $(c)_i$, $(c)_{ii}$, $(d)_i$ and $(d)_{ii}$ from the significance of the joint regression, $\bar{\beta}$ from one and of the joint remainder.

Item	d.f.	$(b)_i$	$(b)_{ii}$	$(c)_i$	$(c)_{ii}$	$(d)_i$	$(d)_{ii}$
				1981			
$\bar{\beta}$		0.97	0.99	0.87	0.94	0.76	0.99
$\bar{\beta}$ -1		-0.03	-0.01	-0.13	-0.06	-0.29	-0.01
Joint remainder	14	147.62	112.77	204.64	193.17	463.73**	64.36
Error	3021	251.72	251.72	251.72	251.72	251.72	251.72
				1982			
$\bar{\beta}$		0.94	0.89	0.94	0.87	0.77	0.96
$\bar{\beta}$ -1		-0.06	-0.11	-0.06	-0.13	-0.23	-0.04
Joint Remainder	14	94.37	194.66	74.66	224.31	693.32**	149.46
Error	3021	201.76	201.76	201.76	201.76	201.76	201.76

,* Significant at 1% and 0.1% level respectively.

Table 39: Significance of the heterogeneity of regression and of the heterogeneity of remainder using the environmental assessors $(b)_i$, $(b)_{ii}$, $(c)_i$, $(c)_{ii}$, $(d)_i$ and $(d)_{ii}$.

Item	d.f.	$(b)_i$	$(b)_{ii}$	$(c)_i$	$(c)_{ii}$	$(d)_i$	$(d)_{ii}$
				1981			
Heterogeneity of Regression (P)	2	1124.61**	1020.76**	1732.14***	1476.79**	695.16	1894.06***
Heterogeneity of Remainder (P)	28	632.94***	490.70***	697.55***	932.14***	722.00***	1123.04***
Heterogeneity of Regression (I)	59	1065.93***	1476.11***	605.32***	1227.09***	765.83***	1604.41***
Heterogeneity of Remainder (I)	826	732.19***	924.06***	991.49***	927.14***	1124.06***	913.66***
Error	3021	271.65	271.65	271.65	271.65	271.65	271.65
				1982			
Heterogeneity of Regression (P)	2	1661.42**	1032.40*	1272.00**	1822.49***	691.64	1473.33**
Heterogeneity of Remainder (P)	28	1193.74***	664.66***	1029.33***	674.05***	1021.40***	923.66***
Heterogeneity of Regression (I)	59	1409.34***	1237.55***	1607.75***	1479.00***	917.23***	1827.16***
Heterogeneity of Remainder (I)	826	921.76***	876.34***	646.93***	891.55***	419.66***	944.33***
Error	3021	251.72	251.72	251.72	2.51.72	251.72	251.72

*, **, *** Significant at 5%, 1% and 0.1% level respectively.

Table 40: Rank correlation over the 60 inbred lines between their regression coefficients with the dependent environmental assessment, $1 + \beta_d$, and those, $\bar{\beta} + \beta_d$'s, with the different kinds of independent environmental assessments, $(b)_i$, $(b)_{ii}$, $(c)_i$, $(c)_{ii}$, $(d)_i$ and $(d)_{ii}$.

Independent Environmental assessors	d.f.	Rank correlation 1981	Rank correlation 1982
$(b)_i$	58	0.941	0.831
$(b)_{ii}$	58	0.679	0.932
$(c)_i$	28	0.411	0.904
$(c)_{ii}$	28	0.714	0.892
$(d)_i$	58	0.832	0.976
$(d)_{ii}$	58	0.993	0.824

Table 41: The rank correlation over the 60 inbred lines between the average variance within environments, δ^2_w and the linear regression coefficient, β_d (with the dependent environmental component, ej), and the total variance between environments, $\bar{V}_{G+E}$.

	d.f.	1981	1982
Correlation of			
β_d and $\delta^2 w$	58	-0.67^{***}	-0.49^{***}
$\bar{V}_{G+E}$ and $\delta^2 w$	58	$0.09^{n.s.}$	$-0.14^{n.s.}$

n.s. Probability is non-significant.

*** Significant at 0.1% level.

Table 42: Number of effective factors, K, controlling the differences among the 60 inbred lines as measured by the additive genetical component $[d]$, and its linear sensitivity β_d.

K for	1981	1982
$[d]$	7	8
β_d	3	6

Experiment 5:

The 10 inbred lines are a stratified sample of the 60 lines, described in experiment 4. Genotypes in this study, therefore, are treated as a fixed effect together with the environments in the analysis of variance and the regressions have been made against the dependent environmental component ej. The sixteen combinations of nitrogen, phosphorous and potassium are treated separately in the absence and presence of calcium because of the large and obvious difference between these two sets. The mean of each of the 10 inbred lines over different two sets of environments are shown in table 43. This experiment was repeated in two conjugative years in 1981 and 1982. A considerable range of variation was obtained between the two sets of environments.

The analysis of variance has been carried out for the 10 inbred lines in each of the two sets of environments, the latter being the eight fertiliser combinations without calcium, NPK, the eight combinations with calcium, NPKCa. The items for genotypes, environments, and genotype x environments in these analysis are highly significant (Expt. 4, table 36).

Corresponding joint regression analyses have been carried out and the results are given in experiment 4, (table 39). Comparison of this table shows the significances of the regression items for the 10 and 60 inbred lines respectively in the set of environments.

The distribution of the values of regression coefficients (b) in the two years study of 10 inbred lines (table 45) were heterogenous, hence all the 10 inbred lines have different responses to the different environments. The incidence of the genotype-environmental interaction and the relative magnitudes of its linear and non-linear components differ markedly over the two sets of environments, with calcium and without calcium.

The actual regression lines are shown in figure 4. To avoid confusion, individual points are not plotted, crossing of regression lines is one of the common features of the graph in the years 1981 and 1982. Differences of the 10 inbred lines were very marked in NPK compared to NPKCa.

The estimates of the additive genetical component, [d], and the linear regression coefficient, β_ds of the 10 inbred lines and of the mean, m, in the two sets of encironments are given in table 44 and 46. The mean performance in each environmental set ($\hat{m}$ of table 44), which differ significantly over sets for two years, show that the coleoptile length was reduced in the NPKCa set in the year 1981 but were reduced to a lesser extent in the year 1982 compared with the NPK set in both the years. Using $\hat{m}$ as the measure of the average quality of the environments within a set (table 44 and 46), shows that the poorer the environments within a set, the more significant are the differences among the linear and non-linear interaction components of the 10 inbred lines. Equally, the

poorer the environments the greater the positive relationship between the additive genetical component, $[d]$, and the linear regression coefficient, βd, over the inbred lines.

The specificity of the genotype-environmental interaction in the two environmental sets, the rank correlations (for 8 degrees of freedom) between δ^2_w and βd and and $\bar{V}_{G+E}$, comparable to those of the 60 inbred lines given in experiment 4, table 41, have been calculated for the 10 inbred lines in each of the two sets. The significant rank correlations shown in table 47 are all positive in the two years study and there is perfect agreement, for every combination of environmental set, in the significance of corresponding rank correlation between δ^2_w and βd and δ^2_w and $\bar{V}_{G+E}$.

Table 43: Mean of each of the 10 inbred lines.

Line	1981		1982	
	NPK	NPKCa	NPK	NPKCa
1	59.14	58.32	57.14	59.13
2	69.19	64.23	66.55	69.32
3	65.23	66.55	69.23	71.19
4	75.81	71.19	74.44	78.36
5	71.14	78.23	68.13	67.55
6	55.22	53.32	60.92	54.11
7	79.30	77.05	74.23	78.23
8	82.36	79.11	78.82	79.15
9	49.55	55.26	52.29	56.73
10	66.15	65.79	64.56	68.92
Mean	67.31	66.90	66.63	68.27

Table 44: Estimates of the additive genetical components, [d], of 10 inbred lines.

Line	1981		1982	
	NPK	NPKCa	NPK	NPKCa
1	8.17	8.58	9.49	9.14
2	-1.88	2.67	0.08	-1.05
3	2.08	0.35	-2.60	-2.92
4	-8.50	-4.29	-7.81	-10.09
5	-3.83	-11.33	-1.50	0.72
6	12.09	13.58	5.71	14.16
7	-11.99	-10.15	-7.60	-9.96
8	-15.05	-12.21	-12.19	-10.88
9	17.76	11.64	14.34	11.54
10	1.16	1.11	2.07	-0.65
$\hat{m}$	67.31	66.90	66.63	68.27

Table 45: Regression co-efficient of 10 inbred lines.

Line	1981		1982	
	NPK	NPKCa	NPK	NPKCa
1	1.97	1.72	1.77	1.69
2	0.73	1.36	0.81	1.27
3	0.64	1.22	0.61	1.36
4	1.19	0.53	1.23	0.69
5	1.57	0.91	1.59	0.94
6	1.16	0.23	1.24	0.41
7	0.82	0.67	0.80	0.72
8	0.67	0.64	0.61	0.69
9	0.41	1.45	0.45	1.22
10	0.84	1.27	0.89	1.01

Table 46: Linear interaction co-efficient, βd, for the 10 inbred lines.

Line	1981		1982	
	NPK	NPKCa	NPK	NPKCa
1	0.97	0.72	0.77	0.69
2	-0.27	0.36	-0.19	0.27
3	-0.36	0.22	-0.39	0.36
4	0.19	-0.47	0.23	-0.31
5	0.57	-0.09	0.59	-0.06
6	0.16	-0.77	0.24	-0.59
7	-0.18	-0.33	-0.20	-0.28
8	-0.33	-0.76	-0.39	-0.31
9	-0.59	0.45	-0.55	0.22
10	-0.16	0.27	-0.11	0.01

Table 47: The rank correlation over the 10 inbred lines between δ^2_w and β_d and V_{G+E}, in the two environmental sets, NPK and NPKCa.

Correlation of	Environmental set	1981	1982
β_d and δ^2_w	NPK	0.79**	0.82**
	NPKCa	0.94***	0.87***
V_{G+E} and δ^2_w	NPK	0.83**	0.81**
	NPKCa	0.89***	0.86**

d.f. = degrees of freedom = 8

** = Significant at 1% level

***= Significant at 0.1% level.

Fig. 4: Phenotypic regression of coleoptile length for 10 inbred lines against environment (nutrition) means.

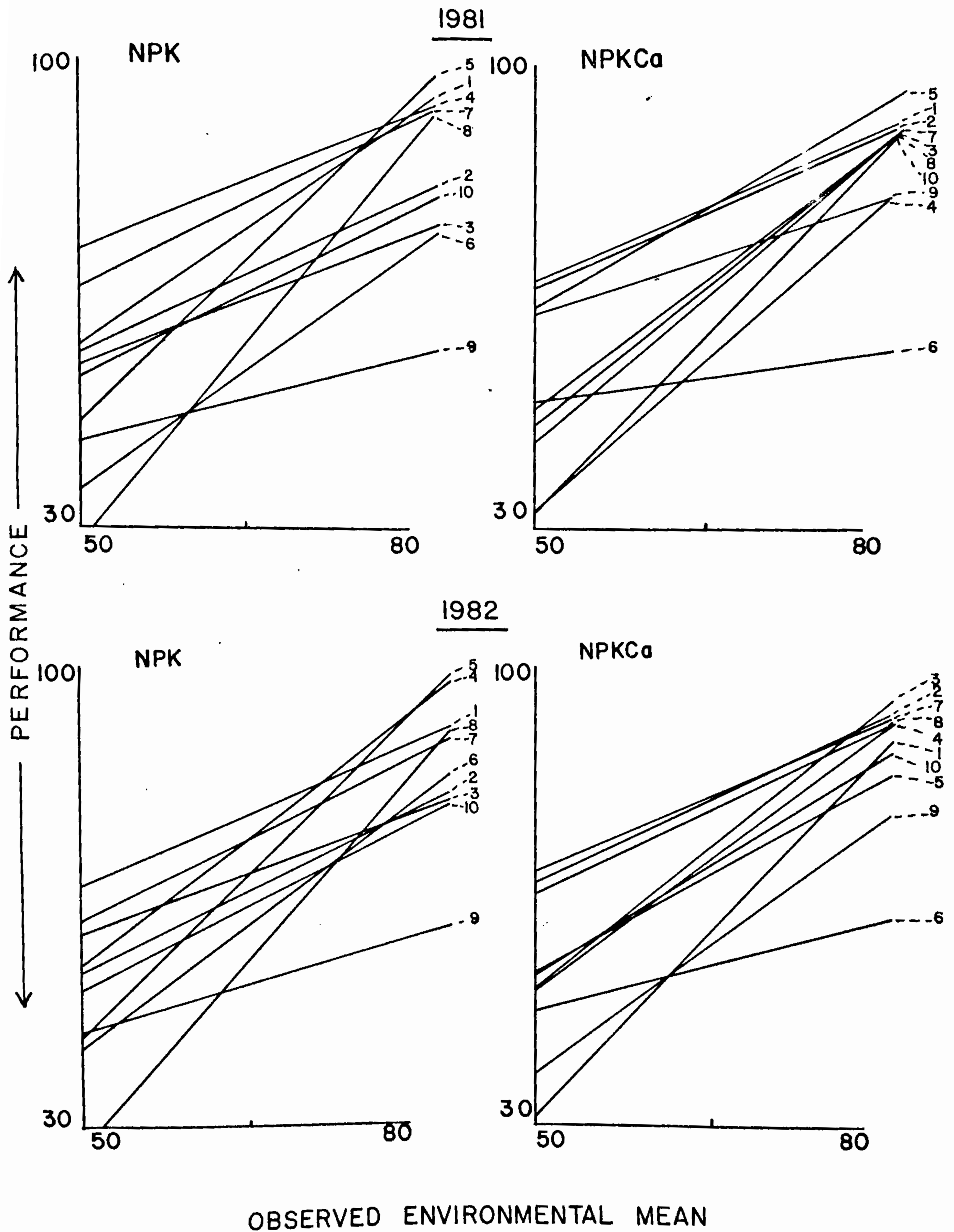


FIG. 4

Experiment 6:

The present investigation is diallel cross analysis involving 10-parents including reciprocals which have been grown in five different temperature environments in order to study the genotype-environment interactions. It can be described under the following main heads.

Graphical Analysis.

Various second degree statistics were calculated from the diallel tables, and from these statistics W_r/V_r and W'_r/W_r graphs were drawn for each of the five environments.

The W_r/V_r graph prospectively provides information on three points. First, it supplies a test of the adequacy of the model in the absence of non-allelic interaction and with independent distribution of the genes among the parents. W_r is related with V_r by a straight regression line of unit slope. Second, given that the model is adequate, a measure of the average level of dominance is provided by the departure from the origin of the point where the regression line cuts the W_r axis. The distance of this point from the origin is $\frac{1}{4}(D-H_1)$; $D > H_1$, when the intercept is positive, i.e. the regression line of unit slope moves upward to the left, intercepting W_r axis above the point of origin, indicates partial dominance, $D = H_1$, where the line passes through the origin, suggesting

the complete dominance and $D < H_1$, when the intercept is negative, i.e. the downward movement of the regression line of unit slope to the right intercepting W_r axis below the point of origin, indicates overdominance. Finally, the relative order of the points along the regression line indicates the distribution of dominant and recessive genes among the parents; the points nearest the origin indicate that the parents contain most of the dominant genes and the points furthest from the origin suggest that the parents consist of an excess of recessive genes.

The completely recessive parents correspond to points at the upper end of the regression line where they cut the limiting parabola, and completely dominant parents to the points at the lower ends the regression line where they cut the limiting parabola. When there is no dominance ($H_1 = 0$), all the array points cluster at single points ($\frac{1}{2}D$, $\frac{1}{4}D$).

The W'_r/W_r graph differs from the W_r/V_r in that it is more obviously affected by asymmetry of gene distribution and this is indicated whether the genes are correlated or not. With gene symmetry the regression of W'_r/W_r is a straight line of a slope of +0.5. When gene asymmetry occurs, parents with common genotypes will fall above the line of +0.5, parents with different or relatively rare genotypes will fall below it.

The W_r/V_r graph for the five different temperature environment such as 20°, 25°, 30°, 35° and 40°C are given in figures 5 and 6 which also include the graph for the pooled data from all the five environments. The graphs provide information on mean dominance, relative dominance of the parents and evidence of epistasis, when present. Since one of the basic assumption in the diallel cross analysis is that epistasis is not operating, it was considered essential to establish the presence or absence of epistasis in each environment. A deviation of the regression slope from unity (b = 1) in the diallel graph generally indicates the presence of epistasis, although other causes such as correlated gene distributions cannot be excluded, the significance of differences in b in each environment was tested by using the t value of $(1-b)S_b$ with n-2 degrees of freedom.

The W_r/V_r graphs for the pooled data from all environments is shown in figure 5. All the array points are within the limiting parabola as expected. The regression of W_r on V_r was significant and significantly different from zero. The regression line drawn deviated from the line of unit slope and passed above the point of origin. This indicates that some of the array shows non-allelic gene interaction and an over all partial dominance. On examination of $W_r - V_r$ values, uniform difference were noted in all the arrays except for array 3 (involving parent Innia- 66). Therefore, W_r/V_r were

calculated after excluding array 3 from the diallel progeny and the graph drawn is shown in figure 6. The regression coefficient was almost unity and highly significant and the regression line drawn was found to have line of unit slope and passed above the point of origin indicating an over all partial dominance. The array point 9 lies very close to the point of origin whereas the array point 4 lies furthest away. It indicates that most of the dominant genes are present in the recurrent parent of array 9, whereas the recurrent parents 4 posses most of the recessive genes in them. On an over all basis the array points group into three classes of which array 9 and 5 lie nearer to the point of origin; array 1, 2, 3 and 4 lies away from the point of origin and 6,7 and 8 lie nearer to $\bar{W}_r\bar{V}_r$ points. Non allelic gene interaction other than complementary type is found to be operating in the parent of array 3.

The examination of the W'_r/W_r graphs for the pooled data from all the five environments of 10-parent and 9-parent are shown in figures 5 and 6. The regression values of W'_r on V_r were significant for both the 10-parent and 9-parent diallel. They were 0.524 ± 0.52 for 10-parent and 0.449 ± 0.021 for 9-parent diallel respectively. The values approached more to the theoretical value (+0.5) and the regression line for 10-parent and 9-parent diallel indicates over all partial

dominance. Distribution of array points were more or less same in both 10-parent and 9-parent diallel.

The W_r/V_r graphs for all the environments (20°, 25°, 30°, 35° and 40^oC) are shown in figure 5 and 6. All the array points are within the limiting parabola as expected. The regression coefficients obtained for environment 20°, 25° and 40^oC were significant and significantly different from zero and not from unity, whereas those for environment 30° and 35^oC were significantly different from zero and from 1 also. The regression lines drawn were different in different environments used in this study. The distribution of array point was found to be scattered in some environment and in others a general pattern emarged as those obtained from pooled data.

W'_r/W_r graphs gave similar information as those obtained from $\bar{W}_r\bar{V}_r$ graphs. In this analysis also some deviation from expectation was noted.

Hayman's analysis of variance:

Hayman's analysis of variance of diallel table for the 10-parents and 9-parents are shown in table 48 and 49. Table 48 indicates the presence of significant additive and dominance components in all the environments. The reciprocal effects, c and d were found significant in some environments. The item replication was non-significant in both the 10-parents and 9-parents diallel in all the environments.

Analysis including all the environments for 10-parents and 9-parents diallel is shown in table 49. The main items a and b were significant when tested against pooled error, (VR^1), against interaction with the replicate error (VR^2) tested against d or Exd (VR^3), and tested against respective interaction with the environments (VR^4). This indicates that additive and dominance variation are present in these diallel, a significant part of which is independent of environmental and reciprocal effects.

All the three b items viz. b_1, b_2 and b_3 were also significant in all the four variance ratios, except VR^4 for b_1 and b_2 of 10-parent diallel, whereas, VR^4 for b_1 of 9-parent diallel were non significant. The items c and d were non significant as there were no reciprocal differences in these diallel except for VR^2 for c in 10-parent and VR^2 for d in 9-parent were significant. It suggested that a number of crosses showed reciprocal differences.

The item environment was significant indicating environmental effects on the expression of additive and non-additive gene in both the 10-parent and 9-parent diallel. The Exa and Exb items were significant in 10-parent and 9-parent diallel which indicated that the gene effects in one environment was different from that of the other. The item Exb_1, Exb_2 and Exb_3 were also significant in both the 10-parent and 9-parent diallel. In 10-parent diallel the item Exc and Exd were highly

significant against pooled error (VR^1) and against interaction with the replicate (VR^2) at 5% and 1% level respectively, whereas in 9-parent diallel their item was non significant.

Components of variation.

The estimates of components of variation and their ratios for 10-parent and 9-parent diallel showing coleoptile length in five different environments are given in table 50. The overall statistics, representing additive (D) and dominence (H_1) effects of genes, were highly significant for 10-parent and 9-parent diallels. But a greater role was played by the additive genetic variation in the inheritance of character coleoptile length in both the diallels. The average degree of dominance was found to be partial as the values of $(H_1/D)^{\frac{1}{2}}$ were lesser than one for both the sets of diallels. The overall values of the ratio $H_2/4H_1$ for 10-parent and 9-parent diallel were greater than its maximum value 0.25, indicating the symmetrical distribution of genes. An excess of recessive genes in 10-parent and dominant genes in 9-parent diallel was noted by the negative and positive value of F respectively. The ratio $\frac{1}{2}F/\ D(D_1-H_2)^{\frac{1}{2}}$ indicated incomplete dominance at all loci rather than complete dominance at some loci and no dominance at others. Higher heritability values were obtained (both in broad and narrow sense) for both the sets of diallels.

Highly significant estimates of D and H_1 were obtained in all the environments which indicates that both additive and dominance components were responsible for the expression of coleoptile length. This confirms the conclusion obtained from the analysis of variance of diallel tables (table 48 and 49). The degrees of dominance ranged from partial dominance in three environments at 30°, 35° and 40°c to slight overdominance in two environments at 20° and 25°c. for both 10-parent and 9-parent diallel respectively. This test confirms that the coleoptile length was strongly influenced by dominance in certain environments. The values obtained for $H_2/4H_1$ = 0.22 at 25°C and 0.24 at 30°C for 10-parent and 0.10 at 20°C and 0.14 at 25°C for 9-parent indicated asymmetry of genes with positive and negative effects at loci showing dominance and the value of 0.32 at 20°C and 0.47 at 35°C and 0.28 at 40°C for 10-parent whereas, 0.35 at 30°C and 0.51 at 35°C and 0.43 at 40°C respectively which were greater than 0.25 indicated the symmetrical distribution of genes. The ratio h^2/H_2, which provides an estimate of the number of effective factors which exhibit dominance, ranged from 1.41 at 25°C to 11.33 at 30°C for 10-parent whereas 1.32 at 25°C to 3.21 at 40°C for 9-parent diallel. The ratio $\frac{1}{2}F/\left[D(H_1-H_2)\right]^{\frac{1}{2}}$ indicated incomplete dominance at all loci rather than complete dominance at some loci and no dominance at others in different environments. The estimated values of both broad and narrow sense heritability were high in most environments for both the 10-parent and

9-parent diallels which range from 21.54 to 90.89 and 72.0 to 90.67 respectively.

In order to obtain some indication of the variation in the dominance components in different environmental conditions, an analysis of variance of $W_r + V_r$ values was carried out using data from all environments from 10-parent and 9-parent diallel (table 51). The environment (E), array (A) and array x environment interaction (AxE) were highly significant in both for the 10-parent and 9-parent diallel. The array variance ratio for 10-parent diallel was 31.07 whereas for 9-parent diallel obtained 46.47, when tested against their respective error ms. The significant array x environment interaction indicates that the relative dominance of the parents varied considerably with the environments.

To study the interaction of the additive and dominance components with the environments, regression coefficients of these components on the environmental means were calculated for 10-parent and 9-parent diallel and tested for significance (table 52). The b value for the additive component ($b = 7.81^{***}$) for 10-parent and ($b = 9.99^{***}$) for 9-parent diallel were significant. However, the b values for dominance were not significantly different from zero ($b = 0.61$) for 10-parent, whereas it was highly significant ($b = -8.09^{***}$) for 9-parent diallel.

The regression analysis for 10-parent and 9-parent diallel (table 52b) confirmed that a significant portion of the additive x environment interaction was accounted for by the linear function of the environmental means. However, both the additive and dominance components for 10-parent and 9-parent diallel showed deviation around their regression slopes, and the variation for the latter was far higher (figure 7) than for the additive component for 10-parent and 9-parent diallel, which indicates that the relationship between the environmental means and the expression of both additive and dominance components is not simple and straightforward.

Table 48: Hayman's analysis of variance of diallel table.

Item	d.f.	20°C	25°C	30°C	35°C	40°C
				10-parent diallel		
a	9	763.14***	497.19***	1023.55***	1976.05***	897.63***
b	45	40.18***	22.38***	16.52***	28.79***	25.68***
b_1	1	61.22***	89.34***	76.44***	55.23***	80.76***
b_2	9	21.55***	17.64***	9.33**	15.76***	9.32***
b_3	35	44.37***	21.69***	16.66***	31.45***	28.32***
c	9	1.39	2.76**	2.11	2.32	1.04
d	36	0.39	2.14***	1.66	1.23	1.19
Replicates	3	0.23	1.94	2.22	1.04	0.97
Error	297	1.19	1.14	3.76	4.45	2.39
				9-parent diallel		
a	8	693.24***	871.55***	1476.33***	1461.11***	984.19***
b	36	30.34***	25.92***	31.65***	34.27***	40.16***
b_1	1	41.29***	56.73***	40.44***	71.67***	61.55***
b_2	8	26.11***	16.29***	27.72***	31.42***	12.06***
b_3	27	31.19***	27.64***	32.49***	33.73***	47.69***
c	8	1.05	0.94	0.14	2.23	2.76
d	28	0.95	1.14	1.39***	1.67	1.84
Replicates	3	1.05	1.22	0.87	0.29	0.88
Error	240	2.32	3.67	1.19	4.44	3.22

** Significant at 1% level.

*** Significant at 0.1% level.

Table 49: Polled analysis over five environments.

Item	d.f.	m.s.	VR^1	VR^2	VR^3	VR^4
			10-parent diallel			
a	9	1063.39	410.57***	830.77***	444.93***	9.46***
b	45	33.12	12.79***	25.87***	13.85***	2.02***
b_1	1	88.06	34.00***	68.79***	36.84***	3.19
b_2	9	12.31	4.75***	9.61***	5.15***	1.47
b_3	35	36.93	14.26***	28.85***	15.45***	2.04***
c	9	4.32	1.67	3.37*	1.81	1.56
d	36	2.39		1.87		
Environment (E)	4	79.66	30.76***	62.23***	20.32***	
Exa	36	112.32	43.37***	87.75***	28.65***	
Exb	180	16.37	6.32***	12.78***	4.18***	
Exb_1	4	27.62	10.66***	21.58***	7.04***	
Exb_2	36	8.39	3.24***	6.55***	2.14***	
Exb_3	140	18.11	6.99***	14.15***	4.62***	
Exc	36	2.76	1.06***	2.16*		
Exd	144	3.92	1.51***	3.06**		
Reps. in E	15	1.28				
Polled error	1485	2.59				

contd.

Table 49 (contd.)

Item	d.f.	m.s.	VR^1	VR^2	VR^3	VR^4
		9-parent diallel				
a	8	923.79	311.04***	1074.17***	468.93***	42.47***
b	36	23.44	7.89***	27.25***	11.89***	2.98***
b_1	1	74.90	25.22***	87.09***	38.02***	5.11
b_2	8	32.26	10.86***	37.51***	16.37***	3.43**
b_3	27	22.63	7.62***	26.31***	11.48***	3.41***
c	8	0.74				
d	28	1.97		2.29*		1.49***
Environment(E)	4	64.07	21.57***	74.50***	32.52***	
Exa	32	21.75	7.32***	25.29***	16.48***	
Exb	144	7.85	2.64***	9.13***	5.95***	
Exb_1	4	14.66	4.94***	17.05***	11.11***	
Exb_2	32	9.39	3.16***	11.15***	7.26***	
Exb_3	108	6.64	2.23***	7.72***	5.03***	
Exc	32	1.11		1.29		
Exd	112	1.32		1.53		
Reps. in E	15	0.86				
Polled Error	1200	2.97				

*,**,*** Significant at 5%, 1% and 0.1% level respectively.

VR^1. Item tested against polled error

VR^2. Item tested against interaction with the replicate error

VR^3. Item tested against d or Exd

VR^4. Item tested against respective interaction with the environment.

Table 50 : Estimates of the components of genetic variation in the five environments.

Components	20°C	25°C	30°C	35°C	40°C	Overall
		10-parent diallel				
D	78.67 ± 3.96	49.36 ±2.76	287.77 ±2.82	216.94 ±3.43	311.05 ±3.65	188.96 ±3.32
H_1	82.34 ± 8.76	91.67 ±6.11	42.55 ±6.23	33.67 ±7.59	60.64 ±8.08	62.26 ±7.35
H_2	104.15 ± 7.16	81.32 ±4.99	40.67 ±5.09	64.09 ±6.21	69.15 ±6.61	76.07 ±6.01
h^2	206.29 ± 4.79	114.76 ±3.34	460.94 ±3.41	139.81 ±4.15	237.79 ±4.43	231.05 ±4.02
F	41.67 ± 9.14	6.92 ±6.37	11.44 ±6.50	-20.33 ±7.91	-61.63 ±8.43	-16.79 ±7.67
E	1.19 ± 1.19	1.14 ±0.83	3.76 ±0.85	4.45 ±1.03	2.39 ±1.10	4.94 ±1.00
$(H_1/D)^{1/2}$	1.02	1.36	0.38	0.39	0.44	0.57
$H_2/4H_1$	0.32	0.22	0.24	0.47	0.28	0.30
h^2/H_2	1.98	1.41	11.33	2.18	3.44	3.04
$\frac{1}{2}F/[D(H_1-H_2)]^{1/2}$	-0.50	0.15	0.25	0.12	0.59	0.16
Heritability (B)	96.58	97.62	97.45	96.40	98.81	95.88
Heritability (N)	21.54	55.14	90.89	83.47	90.24	80.02

Contd.

Table 50 (contd.)

Components	20°C	25°C	30°C	35°C	40°C	Overall
			9-parent diallel			
D	114.16 ±3.96	105.32 ±2.76	187.55 ±2.82	224.55 ±3.43	317.94 ±3.65	212.97 ±3.32
H_1	197.32 ±8.76	119.62 ±6.11	81.76 ±6.23	32.66 ±7.59	29.81 ±8.08	44.19 ±7.35
H_2	81.94 ±7.16	67.32 ±4.99	114.62 ±5.09	67.29 ±6.21	51.14 ±6.61	56.27 ±6.01
h^2	119.32 ±4.79	89.23 ±3.34	215.66 ±3.41	191.74 ±4.15	164.32 ±4.43	156.05 ±4.02
F	31.29 ±9.14	24.77 ±6.37	1.19 ±6.50	-2.32 ±7.91	-14.76 ±8.43	15.74 ±7.67
E	2.32 ±1.19	3.67 ±0.83	1.19 ±0.85	4.44 ±1.03	3.22 ±1.10	5.12 ±1.00
$(H_1/D)^{\frac{1}{2}}$	1.31	1.06	0.66	0.38	0.31	0.45
$H_2/4H_1$	0.10	0.14	0.35	0.51	0.43	0.32
h^2/H_2	1.45	1.32	1.88	2.85	3.21	2.77
$\frac{1}{2}F/[D(H_1-H_2)]^{\frac{1}{2}}$	0.14	0.17	-0.0076	0.01	0.09	-0.15
Heritability(B)	98.09	95.77	98.88	96.21	98.12	95.42
Heritability (N)	81.29	76.42	72.00	81.88	90.67	82.83

Table 51: Analysis of variance for $W_r + V_r$ for the ten and nine arrays in the five environments.

Source	SS	d.f.	m.s.	VR
		10-parent diallel		
Environments (E)	37468.60	4	9367.15	88.25***
Aggays (A)	29678	9	3297.62	31.07***
AxE	41124.96	36	1142.36	10.76***
Reps. in E	1099.35	15	73.29	
Error	13267.50	125	106.14	
		9-parent diallel		
Environment (E)	30921.63	4	7730.41	88.65***
Arrays (A)	32416.07	8	4052.01	46.47***
AxE	41163.04	32	1286.34	14.75***
Reps. in E	997.69	15	66.51	
Error	10464.44	120	87.20	

*** Significant at 0.1% level.

Table 52: Analysis of response of additive (D) and dominance (H_1) components of genetic variation to changes over five environments.

(a) Regression and correlation coefficients between components of genetic variation and the environment means.

Y	b	r
	10-parent diallel	
Additive (D)	7.81***	0.44
Dominance (H_1)	-0.61	0.16
	9-parent diallel	
Additive (D)	9.99***	0.77
Dominance (H_1)	-8.09***	0.78

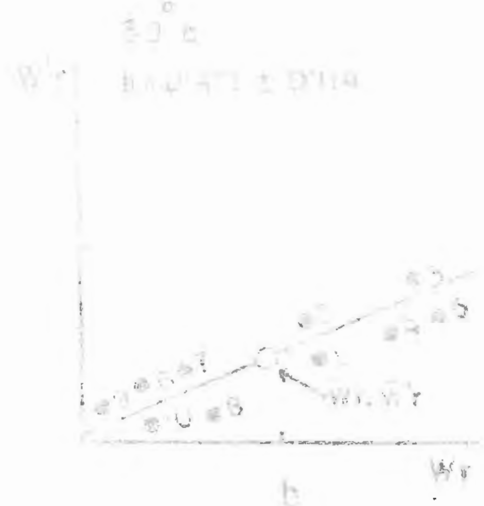
(b) Regression analysis.

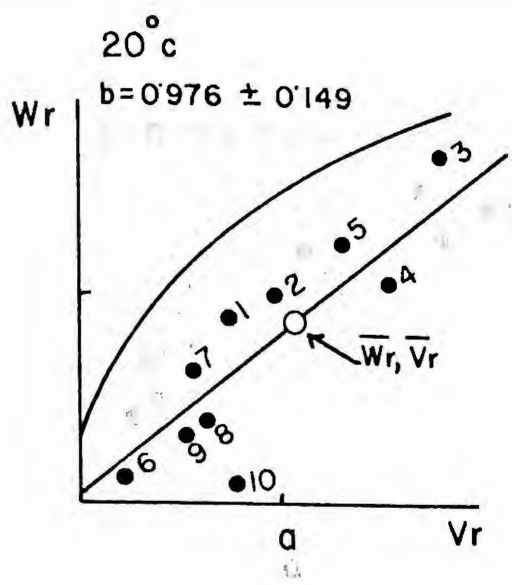
Item	d.f.	Additive (D)	Dominance (H_1)
		10-parent diallel	
Regression	1	1789.62***	2464.76***
Remainder	3	396.55***	1463.75***
Error	1485	2.59	2.59
		9-parent diallel	
Regression	1	2114.09***	1669.73***
Remainder	3	469.15***	921.14***
Error	1200	2.97	2.97

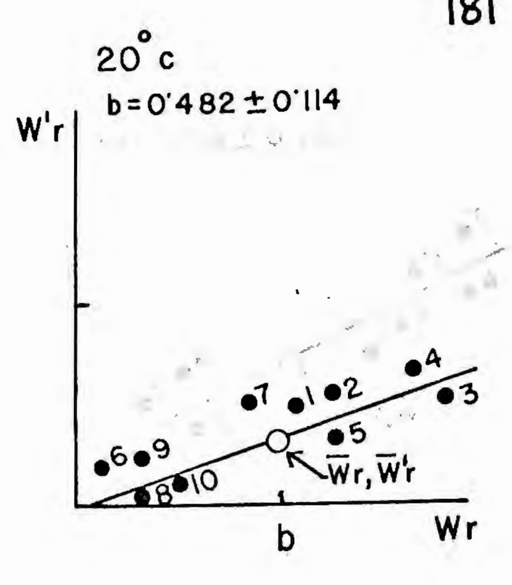
***Significant at 0.1% level.

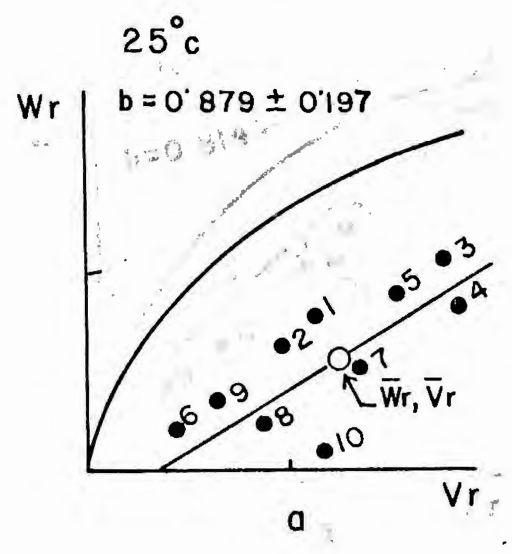
Fig. 5: The W_r/V_r and W'_r/W_r graphs for the five environments and pooled data in 10-parent diallel cross.

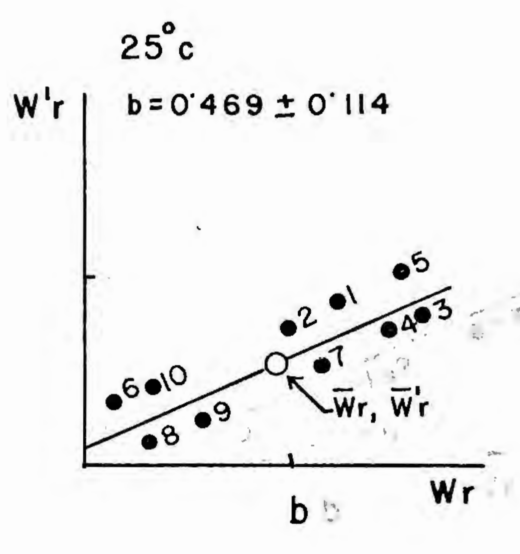
1. Sonora- 64
2. Mexipak- 65
3. Innia- 66
4. Norteno- 67
5. Sonalika
6. Tanori- 71
7. Jupatica- 70
8. Penkty
9. Dirk
10. Kazoli

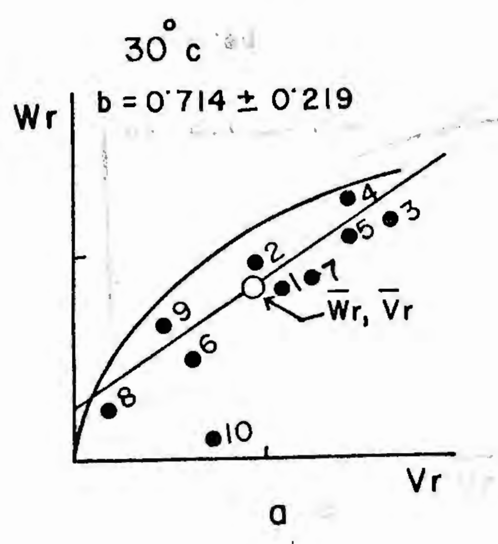












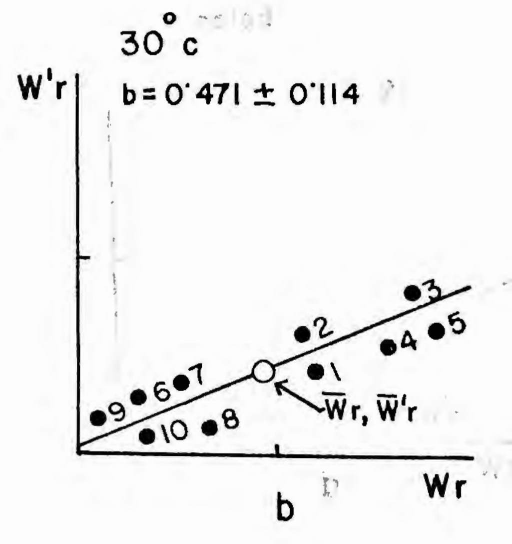


FIG. 5

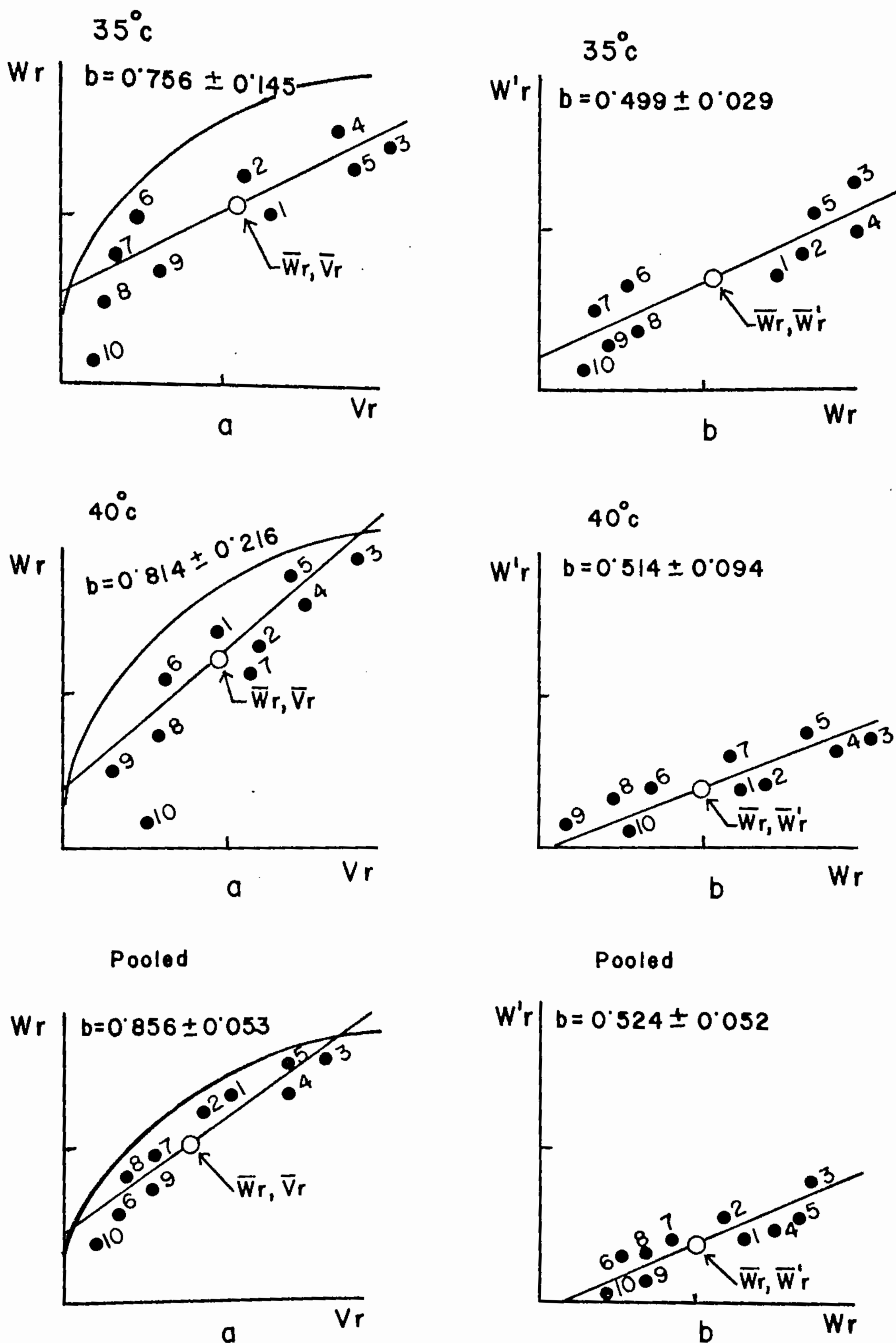


FIG. 5

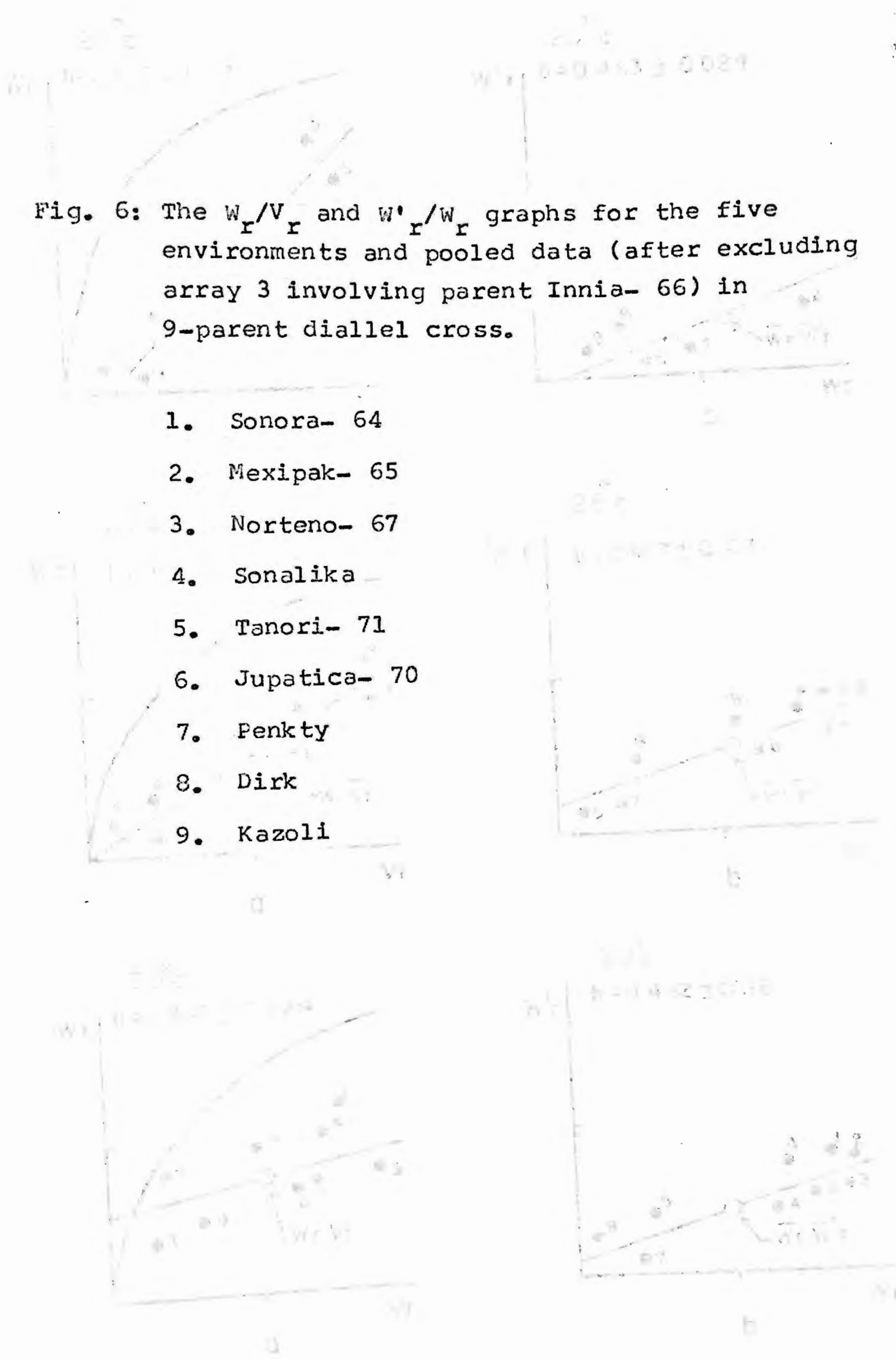
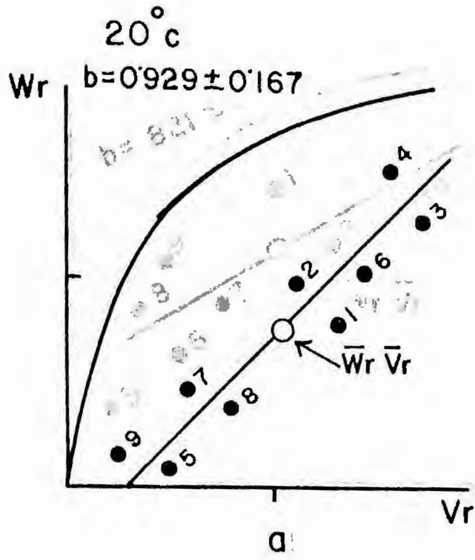
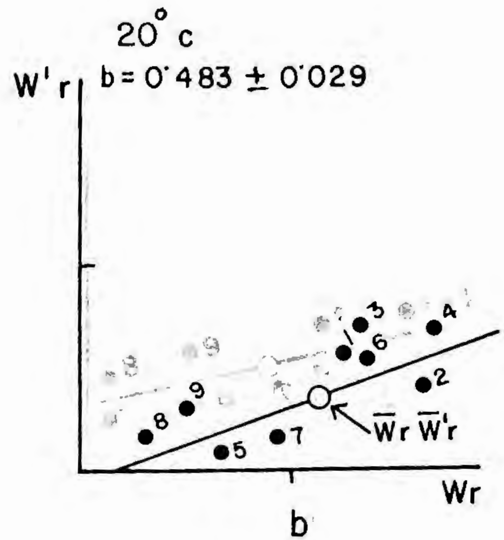
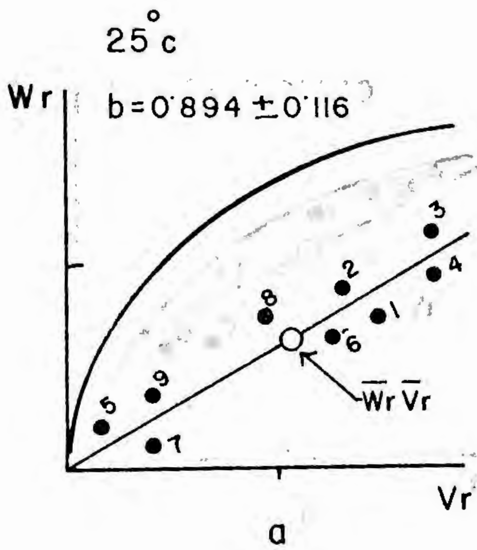


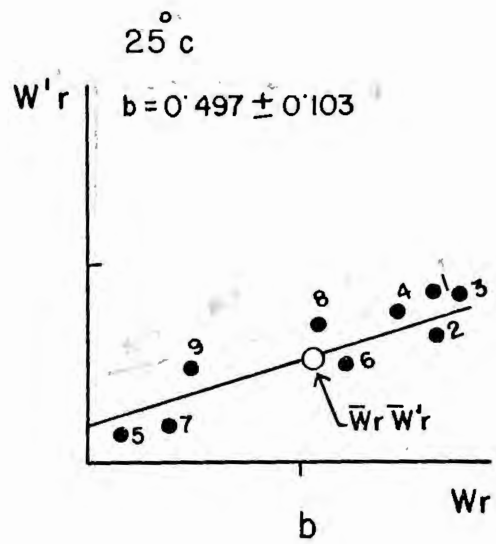
Fig. 6: The W_r/V_r and W'_r/W_r graphs for the five environments and pooled data (after excluding array 3 involving parent Innia- 66) in 9-parent diallel cross.

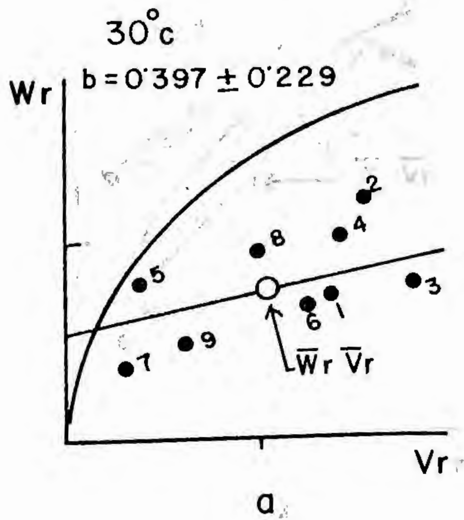
1. Sonora- 64
2. Mexipak- 65
3. Norteno- 67
4. Sonalika
5. Tanori- 71
6. Jupatica- 70
7. Penkty
8. Dirk
9. Kazoli











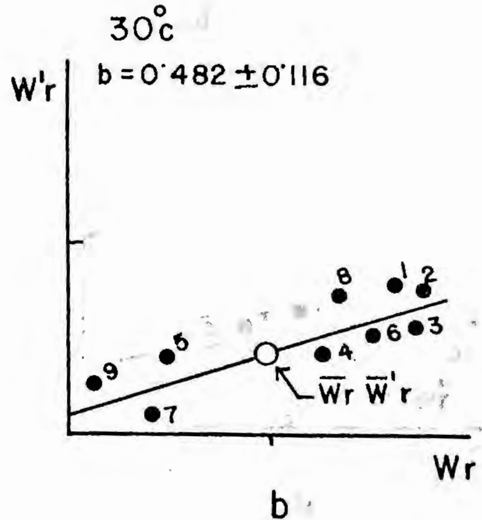
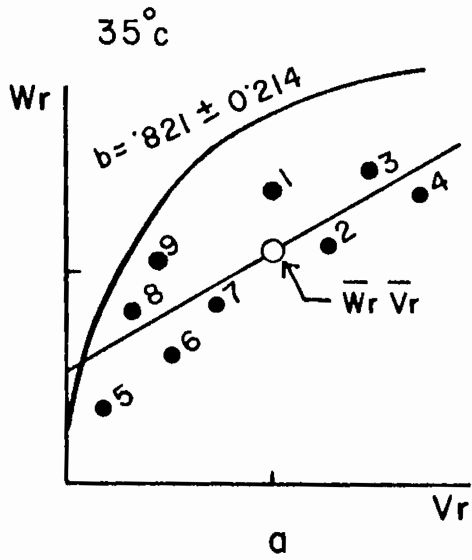
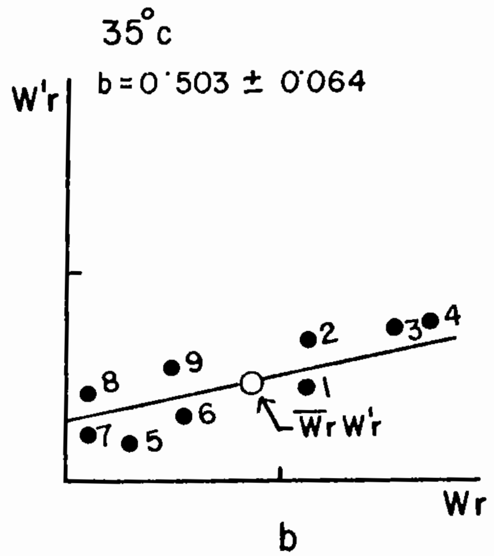
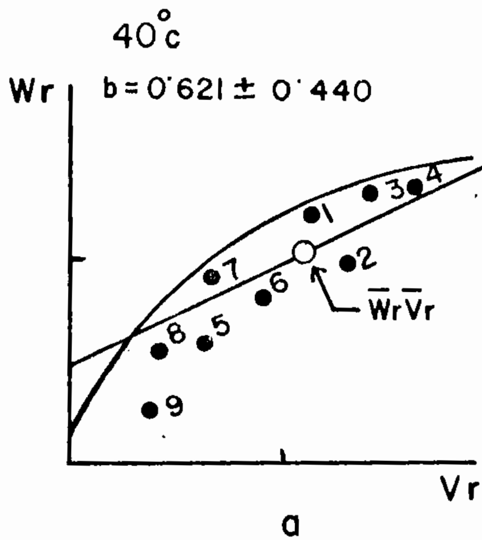
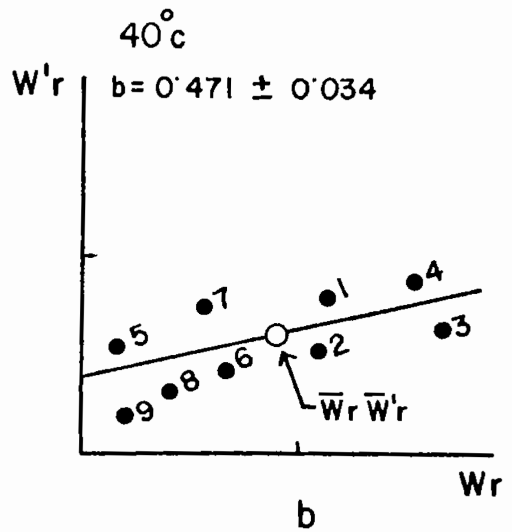


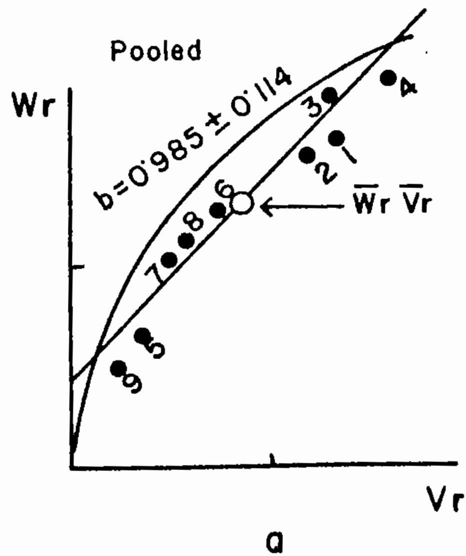
FIG. 6











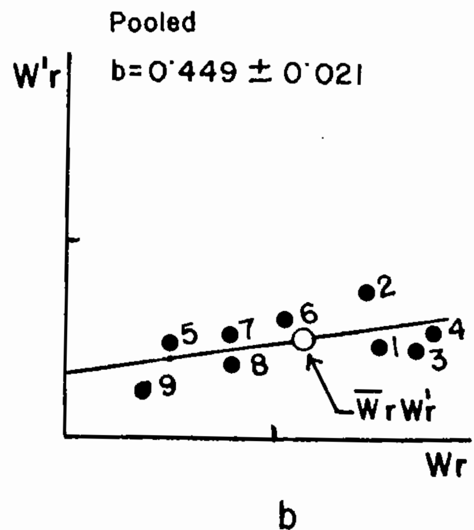


FIG. 6

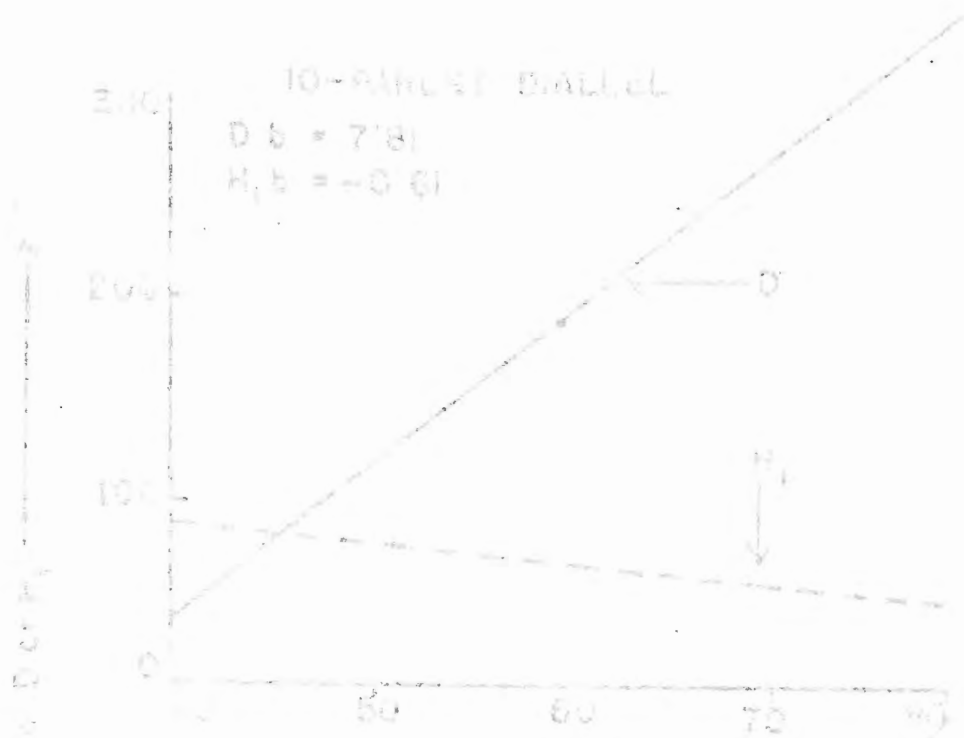
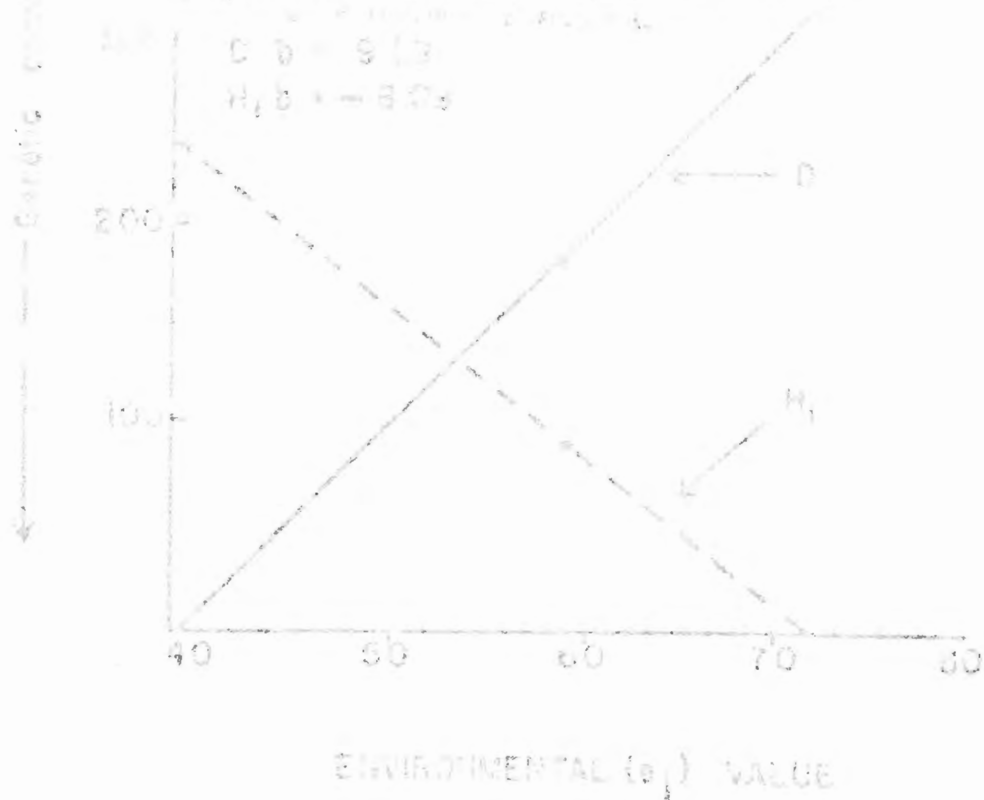


Fig. 7: Regression of the additive and dominance components on environmental means.



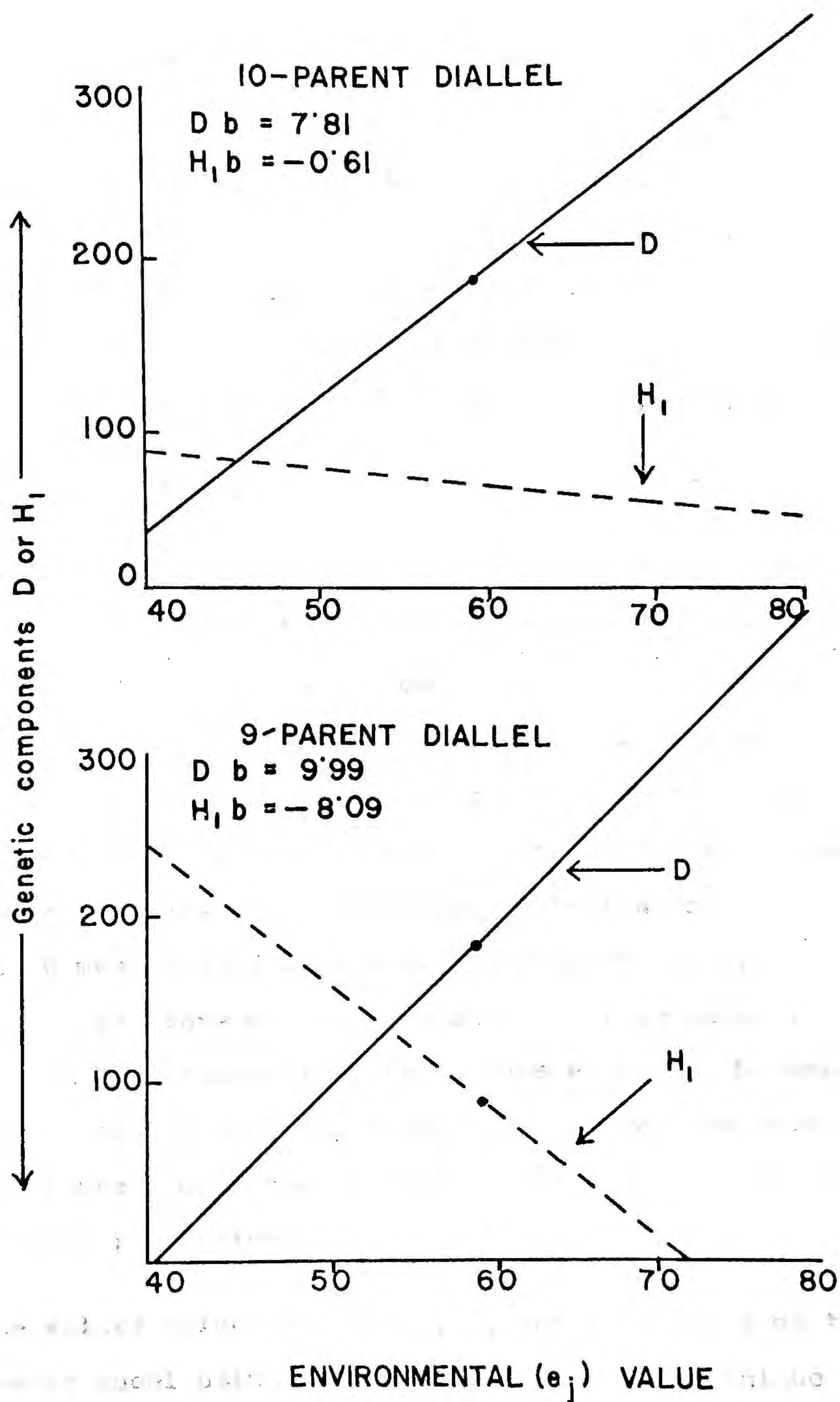


FIG. 7

Experiment 7:

The character coleoptile length which was studied showed continuous variation, indicating polygenic control of the character. Therefore, biometrical techniques of analysis of inheritance of the character was found suitable and was followed. The results obtained from the analysis of a single cross have been described under different heads as follows:

Generation means and epistatic gene effect:

In the absence of epistatis the data fits in a 3-parameter model of Hayman (1958) in which m measures a constant (base population mean); d and h estimate the algebric sum of additive and dominance effects respectively. The values of m, d and h calculated in terms of 3-parameter model are shown in table 53. Then χ^2 test was done to test the goodness of fit of the observed generation means with that of expected generation means based on the 3-parameter estimate. The 6-parameter estimate of the epistatic model is shown in table 54. The estimate d measures additive gene effects, h measures dominance gene effects, i, j and l measures additive x additive, additive x dominance and dominance x dominance epistatic gene effects respectively.

The values calculated for m, d, and h in terms of the 3-parameter model using weighted least square technique for all the crosses are given in table 53. Chi-square (χ^2), values

were significant in most of the crosses except the cross 4 where it was non-significant. Significant χ^2 values suggested the presence of epistasis. The estimate of mean effect (m) was highly significant in all the crosses and was higher in magnitude than those of d and h effects. The additive gene effect (d) was significant for all the crosses. The dominance gene effect (h) was significant in crosses 4,5 and 6 whereas in other it was non-significant. The magnitude of additive gene effect (d) was larger than that of dominant gene effect (h) in most of the crosses. The negative value of h was found in crosses 2,3,4 and 8.

The estimates of m, d and h from 3-parameter model will be biased to an unknown extent by effects not attributable to the additive and dominance action of the genes in those cases where χ^2 values were significant.

As the χ^2 (df.5) estimates under the 3-parameter model were significant, the data were analysed in terms of 6-parameter model to separate the epistatic gene effect from the m, d and h. The weighted least square estimates for m, d, h, i, j and l in terms of 6-parameter model were calculated and the results are shown in table 54. The $\chi^2_{(df.2)}$ was significant in crosses 1,3,6 and 7 indicating that 6-parameter model was not adequate in these cases and that other higher interactions with or without linkage were involved in the mean expression in these crosses. In those crosses where χ^2 values were non-significant

the 6-parameters model was adequate and the estimates of d and h and interaction items were interpretable.

The estimates of mean effect (m) was highly significant in all the crosses and usually greater in magnitude compared to the other estimates. The estimate of additive gene effect (d) was significant in all the crosses except in cross 8. The values of d was larger in magnitude than h in most of the crosses. Significant positive effect of h was observed in crosses 5 and 6 but was negatively significant in cross 2 only.

Total epistatic effects varied in different crosses and were less than the mean effects (m). The estimate of additive x additive (i), was positive and significant in crosses 5 and 7. Significant negative values were observed in cross 2. Additive x dominance (j) effect was significant in crosses 5, 6 and 8 only. Dominance x dominance (l) type of gene action was significant and negative in cross 4 only.

Components of variation:

The unweighted least square estimates of components of variation (D, H, E_1 and E_2) were measured both under inclusive and exclusive analysis and they are shown in table 55. D represents the additive variation, H represents the dominance variation, E_1 and E_2 represent environmental variation.

Inclusive analysis: The estimate of D were positive and significant in all the crosses. The magnitude of D was greater than H in crosses 1,2,6 and 7 respectively. The H estimate was positive and significant in all the crosses except in cross 6 it was non-significant. The estimates of E_1 were positive and significant in all the eight crosses. E_1 estimates were smaller than those of D and H in all the crosses. The magnitude of E_2 was always less than that of E_1. It was non-significant in majority of the crosses.

There were not much differences in inclusive and exclusive estimates of the four quantities, D, H, E_1 and E_2 except in a few crosses where some differences were observed.

Heritability:

Heritability estimates based on components of variation as well as parent-offspring regression are given in table 56. Under inclusive analysis the highest broad sense heritability (HB) was 93.81% in the cross 8 and the lowest was 76.43% in the cross 2. Broad sense heritability was also high under exclusive analysis and ranged from 68.58% to 87.24% respectively in the crosses 2 and 5.

The highest narrow sense heritability (HN) was 68.99% and 68.33% respectively for inclusive and exclusive analysis in the cross 6. The lowest HN was 34.84% in the cross 2 under inclusive analysis and 43.22% in the cross 3 under exclusive analysis.

Heritability estimate from parent-offspring regression is also shown in table 56. This estimate is comparable to that of narrow sense heritability as obtained from components of variation. Therefore, it indicates that a major part of the heritable variation was additive in nature.

Potence and Dominance Ratio:

The degree of dominance h_1, h_2, h_3 and h_4 as it is measured by potence ratio method in the F_1, F_2, F_3 and F_4 generations respectively is shown in table 57.

The potence ratio obtained for F_1, F_2 generations was less than one in most of the crosses except in crosses 5 and 6 where it was more than one. But the h_3 was greater than one in the crosses 1, 2 and 3 whereas, h_4 was greater than one in the crosses 1, 2, 5, 6, 7 and 8 respectively. In the crosses 3 and 4, all the four ratios were negative in nature whereas in the crosses 2 and 6, h_1, h_2, h_3 and h_4 ratios were positive. In cross 1 the h_1, h_2 and h_3 were positive and h_4 was negative and in cross 7, h_1 was positive and h_2, h_3 and h_4 were negative. In cross 8, h_1 and h_2 was negative and h_3 and h_4 was positive.

Degree of dominance as measured by $(H/D)^{\frac{1}{2}}$ from the estimates of both inclusive and exclusive analysis is also shown in table 57. In the crosses 1,2,6 and 7 dominance ratio under both inclusive and exclusive analysis was less than one,

exhibiting partial dominance. In the crosses 3 and 5, by both types of analysis showed overdominance. In the crosses 4 and 8 dominance ratio was greater than one under inclusive analysis whereas it was less than one under exclusive analysis.

Number of Effective Factor:

The number of effective factors were calculated in four different ways and they are shown in table 58.

The number of effective factors calculated as n_1(Castle and Wright, 1921) was less than one in the crosses 4,5,6 and 8 whereas in crosses 1,2,3 and 7 they were 2.11, 2.02, 1.86 and 2.02 respectively. It indicates that at least one to two effective factors are involved in the eight crosses.

The number of effective factors calculated as n_2 (Burton, 1951) also gave similar information as obtained from n_1 estimation. Highest and lowest n_2 values of 2.68 to 0.74 were obtained in cross 1 and 4 respectively.

The estimates of K_1 (Mather, 1949) were less than one in the crosses 5,6 and 8 whereas in crosses 1,2,3,4 and 7 they were 2.46, 2.80, 3.77, 1.03 and 2.43 respectively. From this estimate we can conclude that two to three effective factors are involved in conditioning the coleoptile length in wheat.

The K_2 estimate of Mather (1949) was high in all the crosses. It ranged from 3.27 in cross 4 to 7.82 in cross 7.

Therefore, it can be concluded that three to seven effective factors are involved in this inheritance of coleoptile length of wheat.

To study the interaction of the additive (D), dominance (H_1), additive gene effect (d), dominance gene effect (h), additive x additive effect (i), additive x dominance effect (j) and dominance x dominance effect (l) components with the environments, regression coefficients of these components on the environmental means were calculated and tested for significance (table 59). The b value for the additive component were positive and significant in all the eight crosses, however, the b value for dominance was negative and significant in the crosses 1, 3, 5, 6 and 8, whereas that in the crosses 2, 4, and 7 was positive and significant (table 60). The b value for additive x additive effect was significant in all the crosses. However, crosses 1 and 7 were positive and highly significant, whereas in cross 5 it was negative and highly significant. The b value for additive x dominance effect was positive and significant in the crosses 1,6,7 and 8 whereas other crosses 2,3,4 and 5 were negatively significant. The b values for dominance x dominance effect were positive and highly significant in the crosses 1 and 8 whereas in crosses 3 and 5 it was negatively significant (table 60). The regression analysis (table 59) showed that the additive (D) and dominance (H) components and d, h, i, j, and l effects with

the environments were highly significant. This analysis confirmed that a significant portion of the additive x environment interactions was accounted for by the linear function of the environment means. However, both the additive and dominance components and d, h, i, j and l effects showed deviations around their regression slopes and the variation for the dominance was far higher than for the additive component, which indicates that the relationship between the environmental means and the expression of both additive and dominance components and d, h, i, j and l effects is not simple and straightforward.

Table 53: Estimate of m, d and h based on 3-parameter model.

Cross No.	m	d	h	χ^2
Cross 1	64.55±3.96	10.69±4.67	8.43±8.29	273.66***
Cross 2	65.07±1.07	11.85±1.26	-0.48±2.24	19.95**
Cross 3	66.79±2.09	14.25±2.47	-3.19±4.38	76.41***
Cross 4	65.61±0.53	9.38±0.63	-3.31±1.12	5.06
Cross 5	68.81±1.21	9.29±1.43	14.20±2.53	25.59***
Cross 6	68.08 ±1.88	9.68±2.22	20.36±3.94	61.97***
Cross 7	66.49±1.59	15.73±1.88	0.80±3.34	44.41***
Cross 8	67.06±3.46	4.40±4.08	-6.32±7.24	208.58***
				(d.f. 5)

,* Significant at 1% and 0.1% level respectively.

Table 54: Estimate of m, d, h and the three types of gene interaction (i, j and l) based on 6-parameter model of different crosses.

Cross No.	m	d	h	i	j	l	χ^2
Cross 1	68.59 ± 14.61	13.84 ± 8.49	-14.73 ± 53.99	-2.78 ± 16.02	-31.44 ± 37.96	22.58 ± 47.39	288.34***
Cross 2	68.73 ± 0.94	11.54 ± 0.55	-8.71 ± 3.49	-5.33 ± 1.03	3.07 ± 2.45	4.18 ± 3.07	1.21
Cross 3	69.31 ± 8.01	14.54 ± 4.65	-12.04 ± 29.62	-2.95 ± 8.79	-2.93 ± 20.83	6.95 ± 26.01	86.82***
Cross 4	64.30 ± 0.79	9.01 ± 0.46	3.67 ± 2.95	1.02 ± 0.87	3.75 ± 2.07	-6.65 ± 2.59	0.86
Cross 5	66.34 ± 1.41	8.56 ± 0.82	16.38 ± 5.22	4.31 ± 1.55	7.27 ± 3.67	1.44 ± 4.58	2.70
Cross 6	66.61 ± 2.76	7.61 ± 1.61	20.74 ± 10.22	2.79 ± 3.03	20.70 ± 7.18	2.05 ± 8.97	10.33**
Cross 7	63.65 ± 1.54	14.74 ± 0.89	1.59 ± 5.69	5.34 ± 1.69	9.87 ± 4.01	3.85 ± 5.00	3.21
Cross 8	70.04 ± 7.52	3.31 ± 4.37	-12.28 ± 27.79	-4.50 ± 8.25	-44.11 ± 19.54	2.46 ± 24.39	76.42***
							(d.f. 2)

, * Significant at 1% and 0.1% level respectively.

Table 55: Least square estimates of the components of variation (D, H, E_1 and E_2) of different crosses (1st and 2nd values of a pair correspond to the inclusive and exclusive estimates respectively).

Cross No.	D	H	E_1	E_2
Cross 1	75.29±6.83	67.79±22.84	10.25±3.93	5.04±3.57
	77.79±6.98	45.40±26.35	15.49±5.11	8.41±4.19
Cross 2	45.81±4.77	41.42±15.96	9.87±2.75	1.06±2.49
	47.56±0.71	24.58±2.66	13.71±0.52	1.02±0.42
Cross 3	46.07±5.68	95.99±18.99	7.92±3.27	-1.36±2.97
	48.00±3.40	77.61±12.84	12.12±2.49	-0.74±2.04
Cross 4	74.62±6.67	96.65±22.32	8.23±3.84	2.59±3.49
	78.30±1.55	75.98±5.88	13.55±1.14	-0.08±0.93
Cross 5	87.09±5.94	149.77±19.87	6.16±3.42	-1.41±3.11
	89.56±3.78	127.91±14.27	11.22±2.76	-1.39±2.26
Cross 6	146.88±13.33	41.71±44.59	22.58±7.68	5.86±6.98
	141.89±2.76	70.10±10.45	15.05±2.02	-1.74±1.66
Cross 7	87.21±6.01	55.01±20.09	10.96±3.46	0.61±3.14
	89.27±4.12	36.16±15.56	15.27±3.02	-0.66±2.47
Cross 8	87.57±13.77	133.63±46.04	5.09±7.93	6.69±7.21
	95.98±2.99	80.74±11.31	18.22±2.19	-1.80±1.79

Table 56: Heritability estimates in percentage of different crosses (1st and 2nd values of a pair correspond to the estimates from inclusive and exclusive estimate of components of variation)

Broad Sense Heritability = HB, and

Narrow Sense Heritability= HN.

Parent-offspring Regression= P/O

Cross No.	HB	HN	W_1F_2/F_3	W_1F_3/F_4	W_2F_3/F_4
Cross 1	84.19 76.43	58.05 59.16	71.12	61.32	35.56
Cross 2	76.43 68.58	34.84 54.49	65.11	56.11	32.55
Cross 3	85.58 78.17	41.91 43.22	63.75	47.37	31.87
Cross 4	88.19 81.10	53.52 54.61	70.86	57.86	35.43
Cross 5	92.93 87.24	49.96 50.90	71.44	55.33	35.72
Cross 6	78.78 85.46	68.99 68.33	73.89	70.21	36.94
Cross 7	83.95 77.85	63.82 64.74	73.89	66.34	36.94
Cross 8	93.81 78.91	53.21 55.54	73.51	58.28	36.75

Table 57: Degrees of dominance based on potence ratios (h_1, h_2, h_3 and h_4) method as well as dominance ratio $(H/D)^{\frac{1}{2}}$ method of different crosses.

Cross No.	h_1	h_2	h_3	h_4	$(H/D)^{\frac{1}{2}}$ Inclusive	$(H/D)^{\frac{1}{2}}$ Exclusive
Cross 1	0.73	0.55	2.12	-3.68	0.95	0.76
Cross 2	0.06	0.47	1.25	2.57	0.95	0.72
Cross 3	-0.77	-0.87	-1.18	-0.26	1.44	1.27
Cross 4	-0.45	-0.12	-0.56	-0.16	1.14	0.98
Cross 5	1.56	1.28	-0.27	-2.46	1.31	1.19
Cross 6	2.65	1.83	0.49	1.88	0.53	0.70
Cross 7	0.02	-0.65	-0.97	-2.91	0.79	0.63
Cross 8	-0.59	-0.31	0.57	3.13	1.23	0.91

Table 58: Estimate of number of effective factors based on Castle and Wright, 1921 (n_1); Burton, 1951 (n_2) and Mather, 1949 (k_1), (k_2) for different crosses.

Cross No.	n_1	n_2	k_1	k_2
Cross 1	2.11	2.68	2.46	4.22
Cross 2	2.02	2.01	2.80	6.93
Cross 3	1.86	2.42	3.77	5.12
Cross 4	0.67	0.74	1.03	3.27
Cross 5	0.47	1.05	0.82	4.81
Cross 6	0.31	1.39	0.41	5.99
Cross 7	2.03	2.03	2.43	7.82
Cross 8	0.56	0.66	0.81	6.75

*Estimated from the exclusive estimate of components of variation.

Table 59: Analysis of response of additive (D) and dominance (H_1) components of genetic variation to changes over five encironments. Estimated from the exclusive estimate of components of variation.

Item	d.f.	Cross 1	Cross 2	Cross 3	Cross 4	Cross 5	Cross 6	Cross 7	Cross 8
				D					
Regression	1	1064.31***	2176.05***	3164.00***	1622.10***	44[illegible]2.70***	3076.41***	1922.66***	2367.74***
Remainder	3	219.22***	493.11***	672.09***	917.14***	604.09***	832.32***	411.76***	662.19***
Error	55	14.76	17.11	9.34	21.15	17.03	62.64	55.83	49.84
				H_1					
Regression	1	4003.16***	2976.05***	2073.09***	3041.71***	1830.70***	1416.72***	3461.06***	1996.55***
Remainder	3	917.14***	193.11***	223.06***	1609.22***	421.55***	402.17***	882.15***	288.96**
Error	55	14.76	17.11	9.34	21.15	17.03	62.64	55.83	49.84
				Additive gene effect (d)					
Regression	1	1472.31***	1062.64***	946.44***	874.32***	2219.55***	1764.62***	1417.55***	1926.74***
Remainder	3	644.88***	392.81***	114.17***	227.64***	792.95***	614.56***	444.22***	661.55***
Error	55	14.76	17.11	9.34	21.15	17.03	62.64	55.63	49.84
				Dominance gene effect (h)					
Regression	1	932.14***	1674.50***	1493.32***	1162.74***	3176.15***	1776.23***	2145.37***	2296.14***
Remainder	3	127.55***	227.41***	466.23***	402.11***	394.54***	729.93***	691.66***	722.14***
Error	55	14.76	17.11	9.34	21.15	17.03	62.64	55.63	49.84

(contd.)

Table 59 (contd.)

Item	d.f.	Cross 1	Cross 2	Cross 3	Cross 4	Cross 5	Cross 6	Cross 7	Cross 8
				Additive x additive effect (i)					
Regression	1	669.31***	497.74***	2114.76***	1471.55***	2116.15***	1194.32***	1640.59***	1172.32***
Remainder	3	81.95**	104.22**	664.15***	481.22***	823.64***	416.55***	662.22***	714.14***
Error	55	14.76	17.11	9.34	21.15	17.03	62.64	55.63	49.84
				Additive x dominance effect (j)					
Regression	1	1764.66***	1922.41***	907.06***	1904.05***	1866.55***	1422.18***	923.14***	1644.62***
Remainder	3	214.19***	446.69***	221.44***	416.73***	922.33***	664.17***	404.89***	293.36**
Error	55	14.76	17.11	9.34	21.15	17.03	62.64	55.63	49.84
				Dominance x dominance effect (l)					
Regression	1	2214.64***	1074.22***	1934.22***	2237.64***	2916.44***	2114.92***	1532.16***	1934.76***
Remainder	3	417.32***	662.22***	119.14***	1032.22***	1644.19***	922.24***	723.60**	493.22***
Error	55	14.76	17.11	9.34	21.05	17.03	62.64	95.63	49.84

*,**,*** Significant at 5%, 1% and 0.1% level respectively.

Table 60: Regression analysis.

	Cross 1	Cross 2	Cross 3	Cross 4	Cross 5	Cross 6	Cross 7	Cross 8
b_D	4.29**	7.64***	6.12**	4.34*	9.26**	14.22**	6.92***	7.22**
b_{H_1}	-6.22*	2.14**	-11.15***	4.15*	-7.62**	-8.30**	2.22*	-9.14***
b_i	1.19***	1.27*	2.36*	4.11*	-6.14***	-4.94**	3.22**	-4.44**
b_j	2.26*	-2.81**	-3.93**	-6.61*	-2.46**	4.22**	3.29***	3.17*
b_l	9.66***	4.12*	-3.36**	4.22**	-3.69**	4.66**	3.11**	5.17***

*,**,*** Significant at 5%, 1% and 0.1% level respectively.

Experiment 8:

The six parental genotypes and their F_2, F_3 and F_4 generation of six crosses were examined the transmission of known degrees of linear and non-linear functions of the genotype-environmental interactions among parental lines to the advanced generations derived from crosses among them. Five different effects of temperature and two germinating mediums of low and high pH, were used as the environment in this experiment. Results obtained in 1980, 1981 and 1982 are in the following description:

(a) Scaling of data:

In the first step of analysis, the data were subjected to variance analysis separately for each environment and the error variances (replication x genotype mean squares) thus obtained (table 61) were tested for their homogeneity by Bartlett test. The Bartlett's Chi-squares (table 61) were non-significant in all the three years studied which indicated that the nine error m.s. (replication x genotype m.s.) of each of the parent, F_2, F_3 and F_4 generations were homogeneous. Therefore, no transformation of data into log or square root scales were made, and it was decided to consider untransformed data for the rest of the analysis.

(b) Additive environmental components of variation (e_j):

An estimate of the additive environmental component of variation (e_j) was obtained separately for each of the parental, F_2, F_3 and F_4 generations as the mean of the generation in each environment. The environmental values of e_j of different generations in all the three years are shown in table 62. The e_j values obtained from F_2, F_3 and F_4 generations were very similar to that of e_j values obtained from parental generations. The correlation between e_j values of parental generations with that of F_2, F_3 and F_4 generations were respectively 0.958, 0.946 and 0.965 in 1980, 0.981, 0.993 and 0.991 in 1981 and 0.986, 0.989 and 0.991 in 1982 respectively which are highly significant. It indicated that the e_j values of different generations were almost the same and comparison of results obtained for different generations will be valid.

(c) Analysis of parental data:

The mean coleoptile length of the six parental genotypes and the estimates of the additive genetic components (d_i), linear regression (b_i), linear interaction coefficients (β_i) and deviations from linear slopes $\bar{S}^2d$ over different environments for genotypes were measured separately and they are shown in table 63. Genotypic means varied within six genotypes but a close agreement between years was shown by correlation

coefficient of mean coleoptile length in all the three years which were highly significant (0.929, 0.918 and 0.909). The result, presented in the table 63, reflects in all respects the description of the parents given under material. The additive genetic component (d_i) in table 63 showed a considerable range of variation among the parental lines. The two stability parameters b_i and $\bar{S}^2d$ were also different in different genotypes. Highest coleoptile length was noted in Penkty (82.81 mm, 84.26, and 83.95) and lowest noted in Jupatica- 70 (44.99mm) in 1980 and Mexipak- 65 (57.29mm and 54.39mm) in 1981 and 1982.

The correlation between mean and b_i, mean and $\bar{S}^2d$ and b_i and $\bar{S}^2_d$ in each of the three years were -0.0015, 0.0029 and -0.081 in 1980 and -0.012, -0.119 and -0.028 in 1981 and 0.003, 0.076 and 0.154 in 1982 respectively. These non-significant correlations indicate that the three aspects (mean, response and stability) of a phenotype in respect of coleoptile length are independent of each other and under different gene control.

The analysis of variance and joint regression analysis are shown in table 64. The item genotypes were highly significant in all the three years study indicating that the six parents used in the crosses differed significantly in coleoptile length. The item environment (item 2) was also highly significant in all the three years which indicates that the coleoptile length differs in different environment. The item 3 which

measured the genotype x environment interactions was also significant in all the three years result which indicated that genotype x environment interaction is a part of the genetic system of coleoptile length in these population.

Joint regression techniques were followed to partition the genotype x environment interaction sum squares into different items in respect of grouping of the parents. For example, the three parents (Sonora- 64, Sonalika and Janak) classified, having low linear sensitivities to environmental variation, do not differ in their linear regression (item 4 of table 64). Similarly the three parents (Jupatica- 70, Penkty and Mexipak- 65) classified as having high linear sensitivities to the environmental variation also do not differ in their linear regression (item 6 of table 64). Significant difference in linear regression between the 'low' and 'high' groups were found (item 8 of table 64). There were also significant non-linear components of the genotype x environment interactions within both groups of parents (item 5 and 7 of table 64). The two groups also differ significantly in respect of their non-linear components of genotype x environment interactions (item 9 of table 64) in the year 1980 but it was non-significant in 1981 and 1982.

The actual performance of each genotype over a range of environments is graphically represented in figures 8(A), 9(A) and 10(A) respectively. The regression coefficients b_i are

in effect measures of responses to increments in an improving environment. Since these increments were measured by the mean of all populations, then the average response for any set of populations under consideration must have a regression coefficient of 1.0. The genotypes Jupatica- 70, Penkty and Mexipak- 65 had an average response (b = 1.46, 1.25 and 1.32 in 1980 and 1.34, 1.30 and 1.49 in 1981 and 1.42, 1.38 and 1.59 in 1982 respectively) of which Penkty showed a consistantly greater coleoptile length in all environments whereas Jupatica- 70 and Mexipak- 65 had a greater coleoptile length in good environments only, but a comparatively shorter coleoptile length in unfavourable environments as these two genotypes showed high b_i values and low coleoptile length in this range of environment. The genotypes Sonora- 64, Sonalika and Janak had a response (b = 0.67, 0.71 and 0.59 in 1980 and 0.72, 0.64 and 0.51 in 1981 and 0.61, 0.42 and 0.58 in 1982 respectively) well below the average ($b < 1.0$) and adapted to environments which reduced growth of coleoptile in Penkty, Mexipak- 65 and Jupatica- 70. Figure 8(A), 9(A) and 10(A) showed a marked crossing of regressing lines, a clear indication of a complex genotype x environment interaction present in the coleoptile length of wheat.

(d) The analysis of F_2 data:

Mean coleoptile length of F_2 generations of the six crosses is shown in table 65. Highest coleoptile length was

found in cross 6 in all the three years and the lowest was found in cross 4 in 1980 and in cross 2 in 1981 and 1982. The estimates of three components d_i, b_i and $\bar{S}^2d$ for each of the six crosses in the F_2 generations are shown in table 65. These estimates in all the three different years result have indicated that the difference in coleoptile length and in linear (b_i) and non-linear ($\bar{S}^2_d$) environmental sensitivities among the six parents consistently reflected in the properties of F_2 generations of the six crosses.

The correlation coefficients between mean and b_i, mean and $\bar{S}^2_d$ and b_i and $\bar{S}^2_d$ were 0.021, -0.013 and -0.093 in 1980, 0.003, 0.017 and -0.024 in 1981 and 0.025, 0.031 and 0.073 in 1982. These correlations were also non-significant as found in the parental generations. Therefore, the parental relations among mean, stability and response are also maintained in the F_2 generations.

The analysis of variance and the joint regression analysis of the F_2s of the six crosses were studied and given in table 66. A highly significant g x e interaction effect (item 3 of table 66) was found which indicates that gxe interaction, as found in the parental generations, is also maintained in the F_2 generations. Table 66 also indicates that a portion of the total genetic variation of the F_2 generation is independent of the environmental condition (item 1 of table 66). Significant effect of environment (item 2 of table 66) on the coleoptile length of the F_2 progenies of the

six crosses was indicated. It suggested that the coleoptile length in different environments were different.

On the basis of the parental properties the six crosses have been partitioned into three comparisons by the joint regression analysis by grouping the two crosses between a pair of low parents (cross 3 and 4), the two crosses between a 'high' and a 'low' parent (cross 1 and 2) and the two crosses between a pair of 'high' parents (cross 5 and 6). Within each of these three sets of two crosses there was no significant differences between the linear regressions (item 4, 6 and 8) but there were significant differences between the three sets (item 10 of table 66). There were again significant non-linear components of the interactions within all the three sets (item 5, 7 and 9 of table 66).

The actual performance of the six crosses over a range of environments are presented graphically in figures 8(B), 9(B) and 10(B). A distinct parental property in respect of gxe interactions is reflected in the graph (figure 8 B , 9B and 10B.) The two crosses between a 'high' and a 'low' parent (cross 1 and 2) had a regression slope almost equal to 1.0 (b = 1.06 and 1.02 in 1980; 1.12 and 1.08 in 1981 and 1.09 and 1.02 in 1982 respectively in crosses 1 and 2), properties of average response to different range of environments were reflected. The two crosses between a pair of 'high' parents

(cross 5 and 6) had a steeper slope (b = 1.24 and 1.35 in 1980, 1.31 and 1.22 in 1981 and 1.36 and 1.29 in 1982 respectively in crosses 5 and 6) which means that the coleoptile length of these two crosses were greater in good environment and shorter in poor environments. The two crosses between a pair of 'low' parents (cross 3 and 4) showed a regression slope less than 1.0 ($b < 1.0$) (b = 0.71 and 0.62 in 1980, 0.64 and 0.63 in 1981 and 0.71 and 0.53 in 1982 respectively in crosses 3 and 4) like that of the parents showing that it will have greater coleoptile length in environments where the other four crosses will have low coleoptile length (figure 8B, 9B and 10B). Crossing of regression lines is found in case of parental genotypes in poor environments but spreads out rapidly as the environment improves. This indicates that the difference between genotypes will be more pronounced in good environments.

(e) The analysis of F_3 data:

The data were subjected to variance analysis and the genotype x environment interactions in the six crosses were partitioned by the joint regression techniques. In this analysis the 30F_3 families of each cross were considered separately. In addition to all items as measured for F_2 generations for each of the six crosses, we have, therefore, a heterogeneity of linear regression sum squares comparing the

linear components of 30 families and their remainder sum squares testing the non-linear components. The full analysis of variance and joint regression analysis are presented in table 68. The pattern is quite clear and consistent as those of parent and F_2. A highly significant gxe interaction was found (item 3 of table 68). A significant portion of the total genetic variation present between the crosses is independent of environmental condition (item 1 of table 68).

On the basis of the parental properties the six crosses have been partitioned into three comparisons by the joint regression analysis as done in case of F_2 generations. No significant differences between the linear regression between the two crosses of 'low' x 'low' parents (cross 3 and 4) and between 'high' x 'high' parents (cross 5 and 6) were found (item 17 and 19 of table 68). Significant difference between the linear regression of the two crosses of 'high'x 'low' parents (cross 1 and 2) were found (item 21 of table 68). It indicates that the three 'low' parents (Sonora- 64, Sonalika and Mexipak- 65) differ genetically from each other though they have the same response to environments. There were significant differences between the linear regression of the three sets of crosses, i.e., 'low' x 'low', 'low'x 'high' and 'high' x 'high' (item 23 of table 68). There were significant non-linear components of gxe interactions of the two sets 'high' x 'high' 'low' x 'low' crosses (item 18 and 20 of table 68). No significant non-linear components within the two crosses of

'high x 'low' was found (item 22 of table 68).

There were significant differences among the 30 families for their linear sensitivities to the environment in all the six crosses except in cross 4 in 1980 and crosses 4 and 5 in 1981 and 1982, but the differences were more pronounced in crosses 1 and 2 compared to others where the parents differed in their sensitivities, one being 'high' and the other 'low' (items 4,6,8,10, 12 and 14 of table 68). The significant non-linear components of the interactions were, however, found in crosses 3,4, 5 and 6 in 1980 and 2,3,4,5 and 6 in 1981 and 1982 (items 5,7,9,11,13 and 15 of table 68).

The mean coleoptile length of F_3 generations of the six crosses are given in table 67. Highest coleoptile length was exhibited by cross 6 and lowest by cross 4 in 1980 and by cross 2 in 1981 and 1982. The estimate of the components d_i, b_i and $\bar{S}^2_d$ for each of the six crosses are also shown in table 67. These estimates show that the difference in coleoptile length and in linear (b_i) and non-linear ($\bar{S}^2_d$) environmental sensitivities among the six parents are consistantly reflected in the properties of F_3 progenies of the six crosses.

The correlation coefficients between mean and b_i, mean and $\bar{S}^2_d$ and b_i and $\bar{S}^2_d$ of the six crosses were 0.017, -0.033 and 0.096 in 1980; 0.004, 0.004 and -0.129 in 1981 and 0.007, 0.037 and 0.056 in 1982 respectively. All the three correlations were non-significant as found in parental and F_2

generations. Therefore, these non-significant relations among the three components, mean, stability (b_i) and response ($\bar{S}^2_d$) as found in parents and F_2s are also maintained in the F_3 generations.

The actual performances of the six crosses over a range of environments are represented graphically in figure 8(C), 9(C) and 10(C). Clear parental properties in respect of gxe interactions is reflected in the graph as found in F_2. The two crosses between 'high' and 'low' parents (cross 1 and 2) had a regression slope almost equal to 1.0 (b = 1.12 and 1.06 in 1980, 1.04 and 1.02 in 1981 and 1.02 and 1.08 in 1982 respectively in crosses 1 and 2), a properties of average response over a range of environment was indicated. The two crosses between a pair of 'high' parents (crosses 5 and 6) had a steeper slope (b = 1.19 and 1.25 in 1980; 1.23 and 1.13 in 1981 and 1.17 and 1.19 in 1982 respectively in crosses 5 and 6) and the two crosses between a pair of 'low' parents (cross 3 and 4) showed a regression slope less than 1 ($b < 1.0$) (b = 0.77 and 0.61 in 1980; 0.89 and 0.69 in 1981 and 0.80 and 0.73 in 1982 respectively in crosses 3 and 4). Crossing of regression lines in poor environments and spreading of regression lines in good environments (figure 8C, 9C and 10C) indicates genotype x environment interaction is very common in the six crosses.

The frequency distribution graph of linear sensitivity (b_i) of the $30F_3$ families in the year 1980, 1981 and 1982 are shown in figures 11,12, 13,14,15 and 16 respectively for crosses 1,2,3,4,5 and 6. There was a clear evidence of segregation for differences in linear sensitivity among the families of F_3 generation in cross 1, 2 and 6. Furthermore, these segregations were found to be symetrical around the mean value that corresponds with the mean of the parents of the three crosses.

(f) The analysis of F_4 data:

The data were subjected to a variance analysis and the genotype x environment interaction in the six crosses were separated by the joint regression analysis. The $30F_4$ families of each cross were considered separately in these analyses. In addition to all the items as measured for F_2 and F_3 generations for each of the six crosses we have therefore, a heterogeneity of linear regression sum squares comparing the linear components. The results obtained from analysis of variance and joint regression analysis are shown in table 70. The result is quite clear and consistent as those of F_2 and F_3. Highly significant gxe interactions were found (item 3 of table 69) and a significant portion of the total genetic variation exhibit between the cross is independent of environmental condition (item 1 of table 69).

On the basis of the parental properties the six crosses have been partitioned into three comparisons by the joint regression analysis as done in the case of F_2 and F_3 generations. No significant differences between the linear regression between the two crosses of 'low' x 'low', parents, (crosses 3 and 4) and between 'high' x 'high' parents (crosses 5 and 6) were found (item 17 and 19 of table 69). A significant difference between the linear regression of the two crosses of 'high' x 'low' parents (crosses 1 and 2) was found (item 21 of table 69). This shows that the three 'low' parents (Sonora- 64, Sonalika and Mexipak- 65) differ genetically from each other though they have the same response to environments. There were significant differences between the linear regression of the three sets of crosses i.e. 'low'x 'low', 'low' x 'high' and 'high' x 'high' (item 23 of table 69). There were significant non-linear components of interactions of the two sets, 'high' x 'high' and 'low' x 'low' (item 18 and 20 of table 69). No significant non-linear components within the two crosses of 'high' x 'low' were noted (item 22 of table 69).

There were significant differences among the 30 families for their linear sensitivities to the environment in crosses 1, 2 and 6 in 1980 and 1, 2, 5 and 6 in 1981 and 1,2,3 and 6 in 1982 but the differences were more pronounced in crosses 1 and 2 compared to others where the parents had differing sensitivities, one being 'high' and the other 'low' (items 4,6,8,10,12 and 14 of table 69). Significant non-linear components of the

interactions were, however, found in all the six crosses (items 5, 7, 9, 11, 13 and 15 of table 69).

In table 70 the mean coleoptile length of F_4 generations of six crosses of three different years are given. Highest coleoptile lengths were recorded in cross 6 which were 71.55mm, 77.95mm and 76.29mm in 1980, 1981 and 1982 respectively whereas lowest was recorded in cross 4 (55.30mm) in 1980 and in cross 2 (60.27mm and 52.93mm) in 1981 and 1982. The estimate of the components d_i, b_i and $\bar{S}^2{}_d$ for each of the six crosses is shown in table 70. These estimates show without doubt that the difference in coleoptile length and in linear (b_i) and non-linear ($\bar{S}^2{}_d$) environmental sensitivities among the six parents are consistently reflected in the properties of F_4 generation of the six crosses.

The correlation coefficients between mean and b_i, mean and $\bar{S}^2{}_d$ and b_i and $\bar{S}^2{}_d$ of the six crosses were non-significant. Therefore, it was found that these non-significant relations among the three components, mean, stability and response are also maintained in F_4 generations as found in parental, F_2 and F_3 generations.

The actual performances of six crosses over a range of environments are shown in figures 8(D), 9(D), and 10(D) respectively. Distinct parental properties in respect of gxe interactions is reflected in the graph as found in F_2 and F_3

generations. Crosses 1 and 2 had a regression slope almost equal to 1.0 (b = 1.09 and 1.03 in 1980; 1.09 and 1.08 in 1981 and 1.06 and 1.03 in 1982; respectively in crosses 1 and 2), properties of average response over a range of environment was noted. Crosses 3 and 4 had a regression slope less than 1.0 (b = 0.72 and 0.71 in 1980; 0.81 and 0.72 in 1981 and 0.73 and 0.82 in 1982 respectively in crosses 3 and 4). Crosses 5 and 6 showed a regression slope greater to 1.0 (b = 1.34 and 1.14 in 1980; 1.12 and 1.19 in 1981 and 1.21 and 1.51 in 1982 respectively in crosses 5 and 6). In the graph, diversity of regression lines was not noted but a crossing of regression lines was common which indicates the existence of gxe interactions in these genotypes.

The frequency distribution graph of linear sensitivity (b_i) of the 30F_4 families is shown in figure 11, 12,13,14,15 and 16 respectively for crosses 1,2,3,4,5 and 6. There was a clear evidence of segregation for differences in linear sensitivity among the families of F_4 generations in crosses 1,2 and 6. Furthermore these segregations were found to be symmetrical around the mean value that corresponds with the mean of the parents of the three crosses.

Table 61: Error m.s. of the different environments and the Bartlett χ^2 testing the homogeneity of the different error m.s. of each of the parents, F_2, F_3 and F_4 generations grown under the different temperature environments.

Environment		Parent	F_2	F_3	F_4
		1980			
Control 28°C	Distilled water	4.30	13.12	6.43	7.10
20°C	High pH	3.97	9.83	6.73	7.74
	Low pH	3.53	8.33	6.28	7.19
25°C	High pH	4.26	12.47	6.82	6.79
	Low pH	4.15	10.63	6.68	7.38
30°C	High pH	3.83	10.91	6.79	7.13
	Low pH	4.43	11.47	6.80	6.96
35°C	High pH	3.47	10.44	6.76	7.14
	Low pH	3.80	11.03	6.95	7.28
	χ^2 =	0.207^{ns}	0.621^{ns}	0.207^{ns}	0.207^{ns}
	d.f. = 8				
		1981			
Control 28°C	Distilled water	11.43	4.65	4.03	9.57
20°C	High pH	10.85	4.33	4.19	9.23
	Low pH	12.06	5.58	4.36	9.00
25°C	High pH	10.99	4.84	3.87	9.52
	Low pH	10.51	4.24	4.16	8.90
30°C	High pH	11.22	5.15	4.38	9.17
	Low pH	11.46	3.86	4.22	9.30
35°C	High pH	11.66	4.54	4.26	9.12
	Low pH	11.15	4.64	4.24	9.25
	χ^2 =	0.27^{ns}	0.414^{ns}	0.207^{ns}	0.207^{ns}
	d.f. = 8				

Table 61: (contd.)

Environment		Parent	F_2	F_3	F_4
		1982			
Control 28°C	Distilled water	9.03	9.38	2.80	8.17
20°C	High pH	11.89	10.24	2.99	7.92
	Low pH	9.45	6.04	2.93	8.96
25°C	High pH	10.23	7.93	3.01	8.67
	Low pH	11.52	8.94	3.08	8.76
30°C	High pH	6.44	3.95	2.78	9.68
	Low pH	7.39	9.43	2.75	8.73
35°C	High pH	9.22	10.87	2.97	8.43
	Low pH	9.84	9.64	3.37	8.88
	χ^2 =	1.24^{ns}	1.24^{ns}	0.000	0.207^{ns}
	d.f. = 8				

Table 62: The additive environmental component e_j used in the regression analysis in parents, F_2, F_3 and F_4 generations.

	28°C Distilled water	20°C High pH	20°C Low pH	25°C High pH	25°C low pH	30°C High pH	30°C Low pH	35°C High pH	35°C low pH
				1980					
Parent	-7.69	-11.63	20.41	-1.80	11.73	-17.82	14.79	-20.39	12.42
F_2	-4.89	-15.37	12.93	-4.80	14.62	-12.68	18.02	-16.91	9.03
F_3	-3.69	-17.23	16.94	0.59	3.47	-17.03	10.54	-13.52	14.95
F_4	-7.14	-10.37	13.23	-3.77	13.03	-20.06	12.79	-16.77	19.09
Mean	-5.85	-13.65	15.88	-2.44	10.71	-16.89	14.03	-16.89	13.87
				1981					
Parent	-5.28	-11.78	18.13	-7.57	14.63	-18.96	14.98	-15.26	11.12
F_2	-4.03	-18.06	18.53	-4.47	18.77	-18.08	13.71	-19.56	13.21
F_3	-7.07	-13.59	17.38	-7.10	13.42	-20.85	18.01	-13.48	13.29
F_4	-3.67	-14.93	17.33	-4.45	13.22	-20.71	15.29	-14.31	12.22
Mean	-5.01	-14.59	17.84	-5.89	15.01	-19.65	15.49	-15.65	12.46

Table 62: (contd.)

	28°C	20°C		25°C		30°C		35°C	
	Distilled water	High pH	Low pH	High pH	Low pH	High pH	Low pH	High pH	Low pH
				1982					
Parent	-5.52	-12.12	18.09	-2.91	12.11	-18.95	18.09	-20.00	11.20
F_2	-4.86	-10.31	13.74	-5.27	14.26	-17.29	14.26	-18.26	13.68
F_3	-10.05	-13.80	18.57	-0.41	11.99	-17.92	16.79	-17.43	12.20
F_4	-6.83	-14.75	17.29	-4.25	14.67	-18.44	19.44	-20.41	13.25
Mean	-6.81	-12.74	16.92	-3.21	13.26	-18.15	17.14	-19.02	12.58

Table 63: Mean coleoptile length (mm), additive genetic component (d_i), linear regression (b_i) linear interaction co-efficients, (β_i) and deviation from linear slopes ($\bar{S}^2d_i$) for the six parental lines in the different temperature environments.

Genotypes	Mean	d_i	b_i	β_i	$\bar{S}_d^2$
		1980			
1. Sonora- 64	59.07	-1.99	0.67	0.33	3.62
2. Sonalika	65.58	4.52	0.71	0.29	3.69
3. Janak	62.15	1.09	0.59	0.41	21.44
4. Jupatica- 70	44.99	-16.07	1.46	-0.46	4.59
5. Penkty	82.81	21.75	1.25	-0.25	9.17
6. Mexipak- 65	51.74	-9.32	1.32	-0.32	5.73
Mean.	61.06		1.00		8.04
		1981			
1. Sonora- 64	64.22	-3.25	0.72	0.28	6.27
2. Sonalika	69.24	1.77	0.64	0.36	1.49
3. Janak	71.55	4.08	0.51	0.49	11.22
4. Jupatica- 70	58.26	-9.21	1.34	-0.34	3.24
5. Penkty	84.26	16.79	1.30	-0.30	7.92
6. Mexipak- 65	57.29	-10.18	1.49	-0.49	6.35
Mean.	67.47		1.00		6.08
		1982			
1. Sonora- 64	61.11	-2.39	0.61	0.39	0.29
2. Sonalika	60.25	-3.25	0.42	0.58	2.19
3. Janak	65.05	1.55	0.58	0.42	5.97
4. Jupatica- 70	56.23	-7.27	1.42	-0.42	2.94
5. Penkty	83.95	20.45	1.38	-0.38	15.80
6. Mexipak- 65	54.39	-9.11	1.59	-0.59	6.42
Mean.	63.50		1.00		5.60

Table 64: Analysis of variance (m.s.) and joint regression analysis of gxe interactions for coleoptile length in six parental lines grown in different temperature environments. Figure in the marginal column indicates the item used as denominator in the variance ratio.

Item	d.f.	1980	1981	1982	ms tested against item No.
1. Genotype (G)	5	497.61***	532.44***	617.97***	11
2. Environment (E)	8	764.17***	923.17***	919.93***	11
3. GxE	40	21.83***	16.52***	39.16***	11
<u>Low x Low</u>					
4. Het. of Regression	2	4.63	11.25	22.55	5
5. Remainder	14	16.14***	34.63**	41.67***	11
<u>High x High</u>					
6. Het. of Regression	2	12.97	20.44	12.60	7
7. Remainder	14	23.79***	44.94***	51.32***	11
<u>Low x High</u>					
8. Het. of Regression	1	132.67*	197.60***	105.39**	9
9. Remainder	7	21.32***	11.64	12.67	11
10. Reps. in E	9	4.02	66.11	2.97	
11. Error	45	3.97	11.26	9.45	

*indicates significant at 5% level.

**indicates significant at 1% level.

***indicates significant at 0.1% level.

Table 65: Mean coleoptile length (mm) additive genetic component (d_i), linear regression (b_i) linear interaction coefficients β_i and deviations from linear slopes ($\bar{S}^2d_i$) for the six crosses of F_2 generations in different temperature environments

Cross No.	Mean	d_i	b_i	β_i	$\bar{S}^2_d$
		1980			
Cross 1	69.25	4.15	1.06	-0.06	4.92
Cross 2	57.03	-8.07	1.02	-0.02	2.17
Cross 3	64.73	-0.37	0.71	0.29	8.97
Cross 4	56.92	-8.18	0.62	0.38	14.74
Cross 5	65.11	0.01	1.24	-0.24	4.39
Cross 6	77.57	12.47	1.35	-0.35	6.22
Mean	65.10		1.00		6.90
		1981			
Cross 1	73.22	2.33	1.12	-0.12	8.29
Cross 2	61.53	-9.36	1.08	-0.08	3.11
Cross 3	68.94	-1.95	0.64	0.36	8.76
Cross 4	72.17	1.28	0.63	0.37	6.32
Cross 5	70.55	-0.34	1.31	-0.31	4.22
Cross 6	78.90	8.01	1.22	-0.22	8.97
Mean	70.89		1.00		6.61
		1982			
Cross 1	72.77	5.53	1.09	-0.09	12.71
Cross 2	55.93	-11.31	1.02	-0.02	3.91
Cross 3	63.19	-4.05	0.71	0.29	2.74
Cross 4	60.45	-6.79	0.53	0.47	3.93
Cross 5	73.95	6.71	1.36	-0.36	8.67
Cross 6	77.13	9.89	1.29	-0.29	4.32
Mean	67.24		1.00		6.05

Table 66: Analysis of variance (m.s.) and joint regression analysis of gxe interactions for coleoptile length in six crosses of F_2 generations grown in different temperature environments. Figure in the marginal column indicates the item used as denominator in the variance ratio.

Item	d.f.	1980	1981	1982	ms tested against item No.
1. Genotype (G)	5	329.70***	367.43***	315.11***	13
2. Environment (E)	8	624.19***	899.70***	803.10***	13
3. GxE	40	32.56***	32.90***	37.08***	13
Low x Low					
4. Regression	1	17.29	21.19	8.47	5
5. Remainder	7	51.66***	59.14***	62.34***	13
High x High					
6. Regression	1	96.97	112.13*	141.67*	7
7. Remainder	7	32.97*	19.00*	31.55**	13
High x Low					
8. Regression	1	21.76	9.34	14.75	9
9. Remainder	7	41.73**	50.25***	69.25***	13
Low x High (High x Low)					
10. Regression	2	51.67*	81.55***	59.21***	11
11. Remainder	14	12.74	7.96	4.13	13
12. Reps. in E	9	4.23	3.19	7.26	
13. Error	45	10.92	6.45	8.94	

*indidates significant at 5% level.
**indicates significant at 1% level.
***indicates significant at 0.1% level.

Table 67: Mean coleoptile length (mm), additive genetic component (d_i), linear regression (b_i), linear interaction coefficient, β_i and deviations from linear slopes ($\bar{S}^2 d_i$) for the six crosses of F_3 generations in different temperature environments.

Cross No.	Mean	di	b_i	β_i	$\bar{S}^2_d$
		1980			
Cross 1	71.76	6.97	1.12	-0.12	0.15
Cross 2	59.24	-5.55	1.06	-0.06	4.29
Cross 3	62.15	-2.64	0.77	0.23	12.70
Cross 4	57.13	-7.66	0.61	0.39	19.04
Cross 5	64.93	0.14	1.19	-0.19	6.03
Cross 6	73.55	8.76	1.25	-0.25	7.33
Mean	64.79		1.00		9.26
		1981			
Cross 1	75.14	4.05	1.04	-0.04	7.97
Cross 2	62.67	-8.42	1.02	-0.02	4.50
Cross 3	66.33	-4.76	0.89	0.11	10.24
Cross 4	71.55	0.46	0.69	0.31	7.40
Cross 5	73.94	2.85	1.23	-0.23	6.97
Cross 6	76.93	5.84	1.13	-0.13	6.20
Mean	71.09		1.00		7.55
		1982			
Cross 1	74.77	7.26	1.02	-0.02	14.95
Cross 2	56.60	-10.91	1.08	-0.08	4.98
Cross 3	64.93	-2.58	0.80	0.20	2.16
Cross 4	62.19	-5.32	0.73	0.27	3.93
Cross 5	71.29	3.78	1.17	-0.17	11.23
Cross 6	75.29	7.78	1.19	-0.19	8.24
Mean	67.51		1.00		7.55

Table 68: Analysis of variance (ms) and joint regression analysis of gxe interactions for coleoptile length in six crosses of F_3 generations grown in different temperature environments. Figure in the marginal column indicates the item used as denominator in the variance ratio.

Item	d.f.	1980	1981	1982	ms tested against item No.
1. Genotype (G)	179	297.16***	315.65***	290.10***	26
2. Environment (E)	8	423.60***	556.30***	513.00***	26
3. GxE	1432	24.00***	24.38***	29.07***	26
Cross 1. High x Low					
4. Regression	29	49.34***	69.17***	80.94***	26
5. Remainder	203	2.31	4.17	2.23	26
Cross 2. High x Low					
6. Regression	29	37.66***	47.15***	102.15***	26
7. Remainder	203	5.14	8.97***	3.86***	26
Cross 3. LowxLow					
8. Regression	29	14.16***	21.64***	20.75***	9
9. Remainder	203	9.34***	11.12***	9.15***	26
Cross 4. LowxLow					
10. Regression	29	15.67	22.79	20.55	11
11. Remainder	203	39.50***	41.73***	63.92***	26
Cross 5. High x High					
12. Regression	29	61.22***	40.93	13.67	13
13. Remainder	203	59.04***	48.93***	67.11***	26

Table 68: (contd.)

Item	d.f.	1980	1981	1982	ms tested against item No.
Cross 6. HighxHigh					
14. Regression	29	41.75***	78.92***	60.55***	15
15. Remainder	203	17.50***	14.59***	15.73***	26
16. Crosses x Environments	40	12.22***	12.13***	12.48***	26
Low x Low					
17. Regression	1	16.64	8.25	7.23	18
18. Remainder	7	14.95*	17.16***	11.23***	26
High x High					
19. Regression	1	4.59	11.76	10.29	20
20. Remainder	7	14.93*	18.04**	21.55***	26
High x Low					
21. Regression	1	51.75**	29.76**	71.92***	26
22. Remainder	7	5.73	5.29	1.34	26
Lowx High vs. (High x Low)					
23. Regression	2	29.24*	55.25***	49.33***	26
24. Remainder	14	7.64	2.95	5.16*	26
25. Reps. in E	9	4.32	0.79	1.83	
26. Error	1611	6.73	4.19	2.97	

*indicates significant at 5% level.

**indicates significant at 1% level.

***indicates significant at 0.1% level.

Table 69: Analysis of variance (ms) and joint regression analysis of gxe interactions for coleoptile length in six crosses of F_4 generations grown in different temperature environments. Figure in the marginal column indicates the item used as denominator in the variance ratio.

Item	d.f.	1980	1981	1982	ms tested against item No.
1. Genotype (G)	179	356.01***	404.13***	395.73***	26
2. Environment (E)	8	319.16***	447.05***	502.60***	26
3. GxE	1432	33.19***	35.94***	37.36***	26
Cross 1. High x low					
4. Regression	29	128.16***	97.22***	70.55***	26
5. Remainder	203	18.37***	15.12***	17.34***	26
Cross 2. High x Low					
6. Regression	29	95.23***	61.22***	49.35***	26
7. Remainder	203	9.76***	3.95	7.43***	26
Cross 3. Low x Low					
8. Regression	29	22.76	17.21	34.73***	9
9. Remainder	203	28.24***	51.76***	15.34***	26
Cross 4. Low x Low					
10. Regression	29	18.76	21.70	30.55	11
11. Remainder	203	57.63***	49.00***	73.33***	26
Cross 5. High x High					
12. Regression	29	15.24	67.19***	39.90	13
13. Remainder	203	51.16***	53.93***	76.24***	26

Table 69: (contd.)

Item	d.f.	1980	1981	1982	m.s. tested against item No.
Cross 6. High x High					
14. Regression	29	59.27***	98.16***	88.44***	15
15. Remainder	203	16.23***	12.90***	23.10***	26
16. Crosses x Environments	40	21.69***	30.83***	32.69***	26
Low x Low					
17. Regression	1	14.63	28.00	12.09	18
18. Remainder	7	24.28***	49.17***	47.33***	26
High x High					
19. Regression	1	6.39	16.45	12.32	20
20. Remainder	2	35.64***	51.56***	59.70***	26
High x Low					
21. Regression	1	82.63***	104.10***	95.35***	26
22. Remainder	7	15.13*	27.94**	26.66**	26
Low vs. High vs. (HighxLow)					
23. Regression	2	55.23***	41.63*	29.05***	26
24. Remainder	14	9.14	7.33	8.15	26
25. Reps. in E	9	6.24	1.04	2.38	
26. Error	1611	7.19	9.23	8.76	

*indicates significant at 5% level.

**indicates significant at 1% level.

***indicates significant at 0.1% level.

Table 70: Mean coleoptile length (mm), additive genetic component (d_i), linear regression (b_i), linear interaction coefficient, β_i deviations from linear slopes ($\bar{S}^2 d_i$) for the six crosses of F_4 generations in different temperature environments.

Cross No.	Mean	d_i	b_i	β_i	$\bar{S}^2_d$
		1980			
Cross 1					
Cross 1	70.62	5.89	1.09	-0.09	4.93
Cross 2	59.49	-5.24	1.03	-0.03	3.67
Cross 3	64.32	-0.41	0.72	0.28	13.74
Cross 4	55.30	-9.43	0.71	0.29	12.13
Cross 5	67.10	2.37	1.32	-0.32	4.76
Cross 6	71.55	6.82	1.14	-0.14	5.93
Mean	64.73		1.00		7.53
		1981			
Cross 1	71.54	-0.39	1.09	-0.09	0.11
Cross 2	60.27	-11.66	1.08	-0.08	5.34
Cross 3	68.94	-2.99	0.81	0.19	12.74
Cross 4	75.23	3.30	0.72	0.28	6.20
Cross 5	77.64	5.71	1.12	-0.12	4.14
Cross 6	77.95	6.02	1.19	-0.19	7.95
Mean	71.93		1.00		7.58
		1982			
Cross 1	71.53	4.76	1.06	-0.06	11.22
Cross 2	52.93	-13.84	1.03	-0.03	3.04
Cross 3	63.14	-3.63	0.73	0.27	0.16
Cross 4	62.57	-3.20	0.82	0.18	2.75
Cross 5	74.14	7.32	1.21	-0.21	7.24
Cross 6	76.29	9.52	1.51	-0.51	4.93
Mean	66.77		1.00		4.89

Fig. 8: Regression of individual genotype means on environmental means in 1980.

(A) Parents:

(1) Sonora- 64
(2) Sonalika
(3) Janak
(4) Jupatica- 70
(5) Penkty
(6) Mexipak- 65

(B), (C) and (D) Crosses:

(1) Sonora- 64 x penkty
(2) Sonalika x Mexipak- 65
(3) Sonora- 64 x Janak
(4) Sonalika x Janak
(5) Jupatica- 70 x Penkty
(6) Mexipak- 65 x Penkty

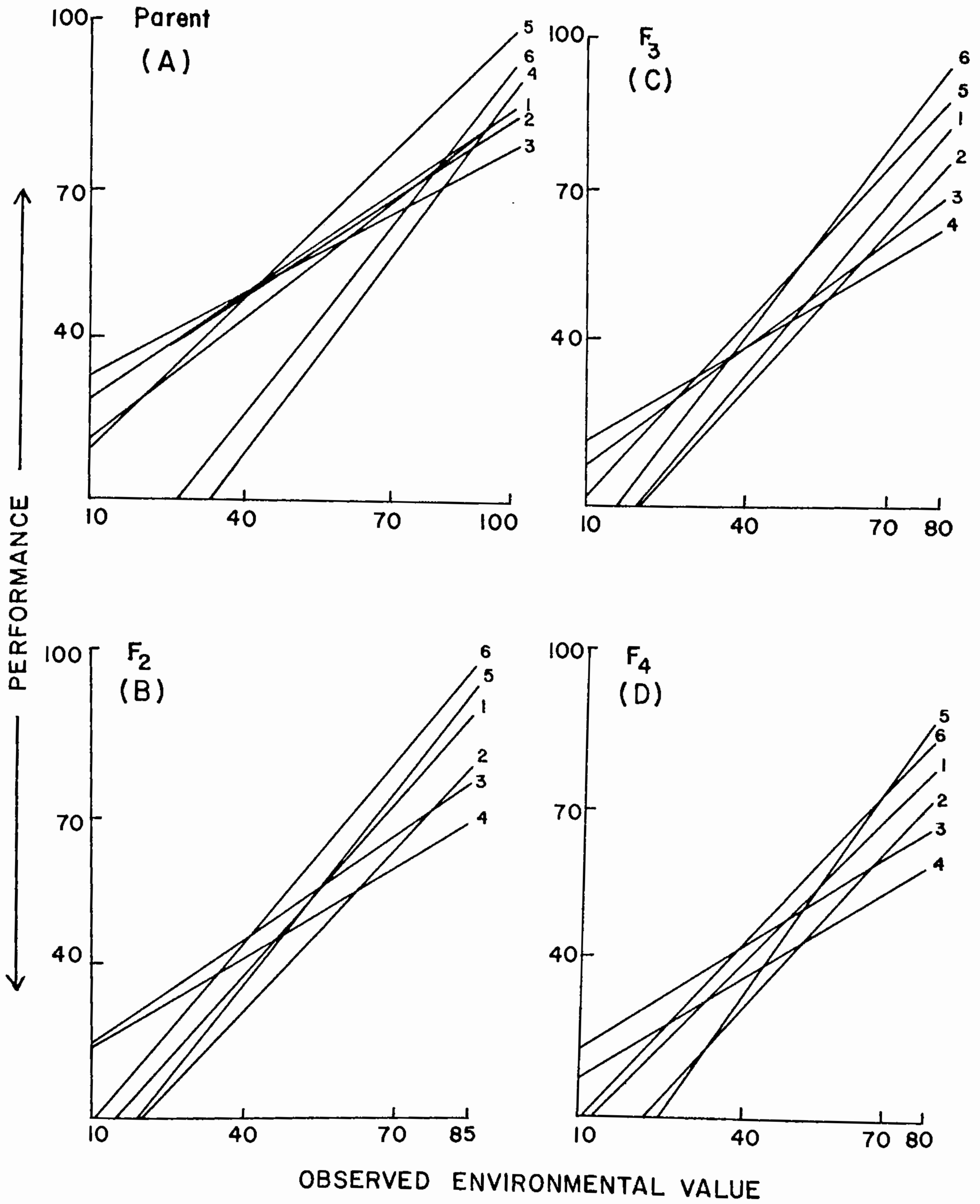


FIG. 8

Fig. 9: Regression of individual genotype means on environmental means in 1981.

(A) Parents:

(1) Sonora- 64
(2) Sonalika
(3) Janak
(4) Jupatica- 70
(5) Penkty
(6) Mexipak- 65

(B), (C) and (D) Crosses:

(1) Sonora- 64 x Penkty
(2) Sonalika x Mexipak- 65
(3) Sonora- 64 x Janak
(4) Sonalika x Janak
(5) Jupatica- 70 x Penkty
(6) Mexipak- 65 x Penkty

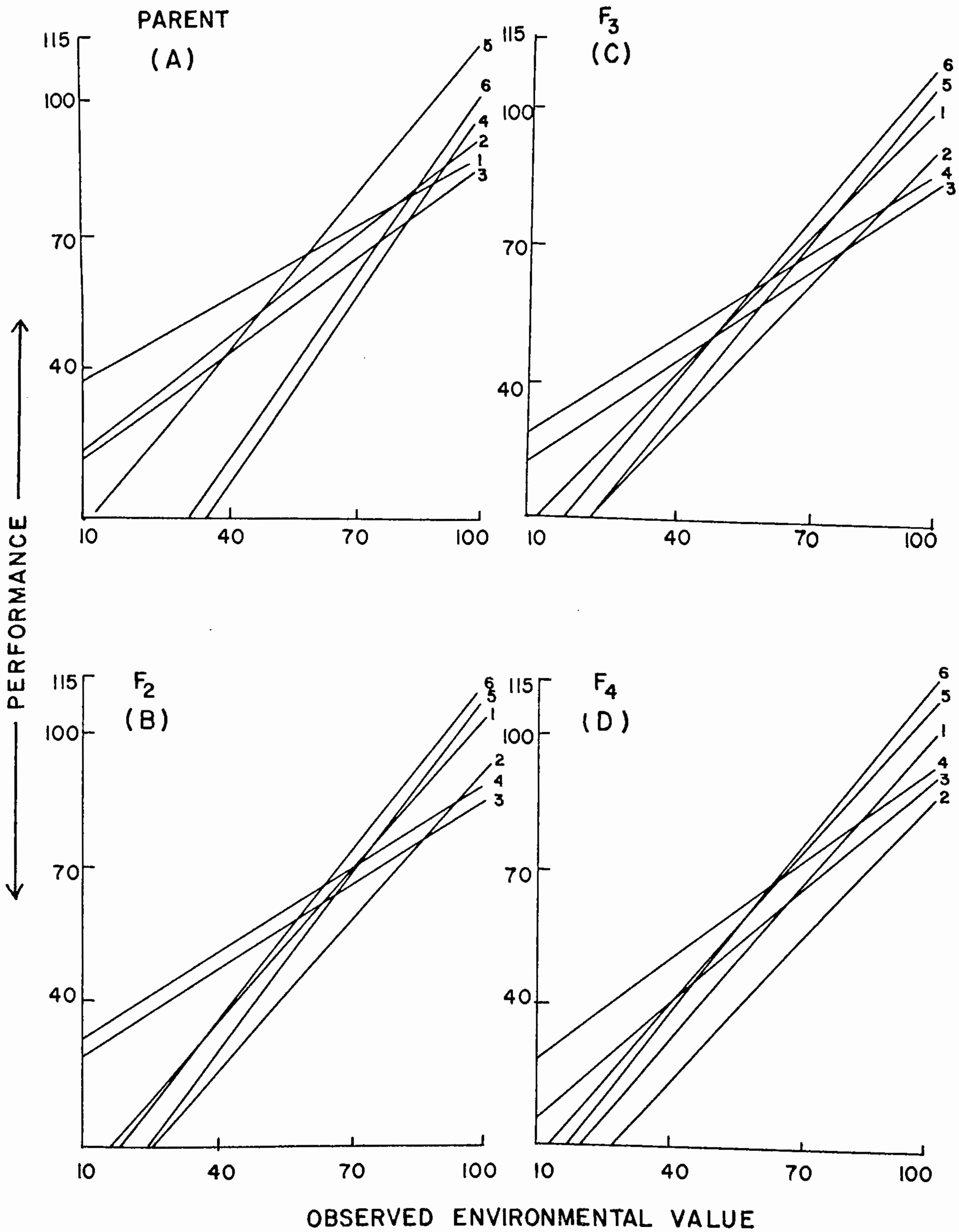


FIG. 9

Fig. 10: Regression of individual genotype means on environmental means in 1982.

(A) Parents:

(1) Sonora- 64
(2) Sonalika
(3) Janak
(4) Jupatica- 70
(5) Penkty
(6) Mexipak- 65

(B), (C) and (D) Crosses:

(1) Sonora- 64 x Penkty
(2) Sonalika x Mexipak- 65
(3) Sonora- 64 x Janak
(4) Sonalika x Janak
(5) Jupatica- 70 x Penkty
(6) Mexipak- 65 x Penkty

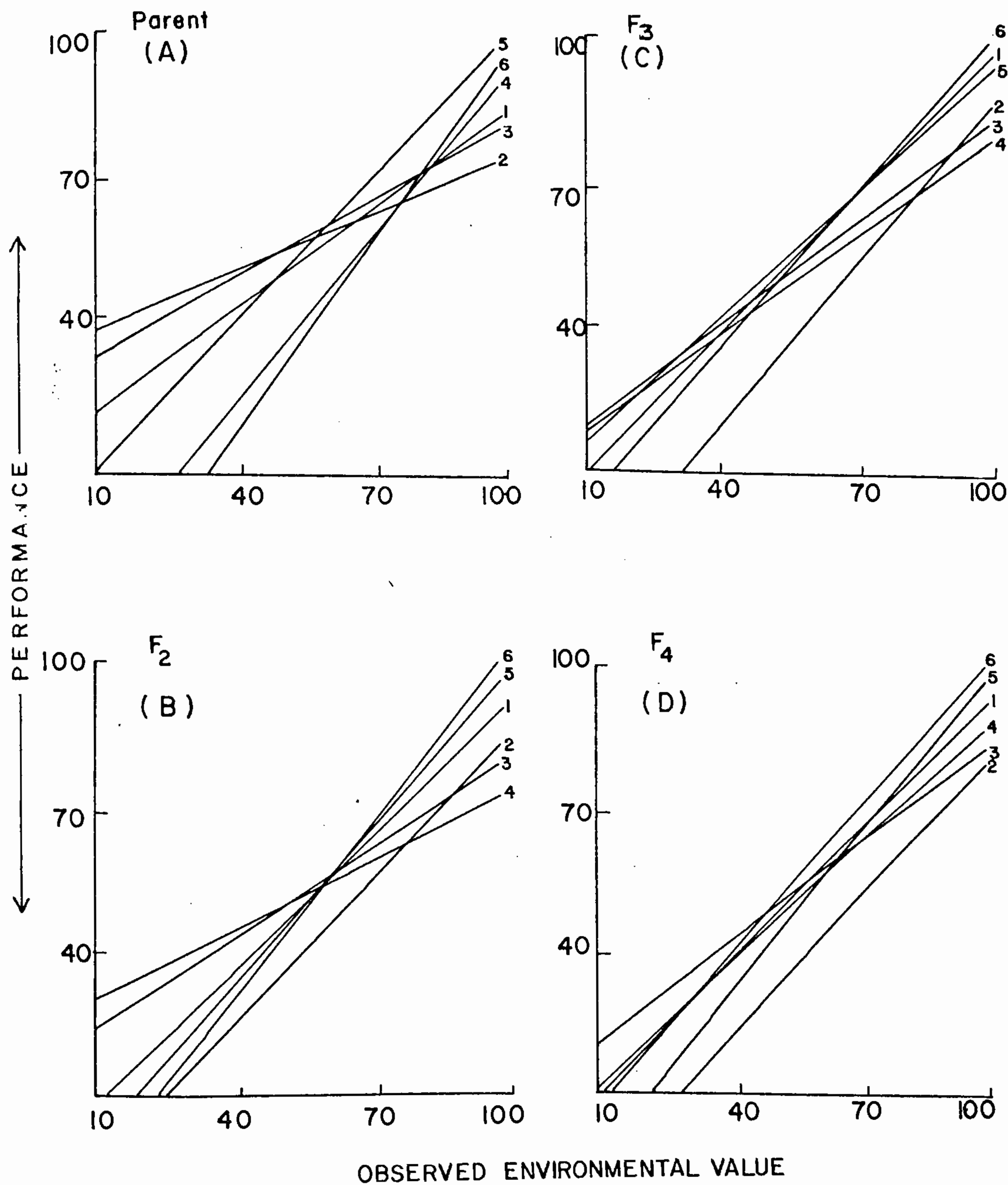


FIG. 10

Fig. 11. Distribution of the linear regression coefficients (b_i) among the 30 families of F_3 and F_4 for the Cross 1.

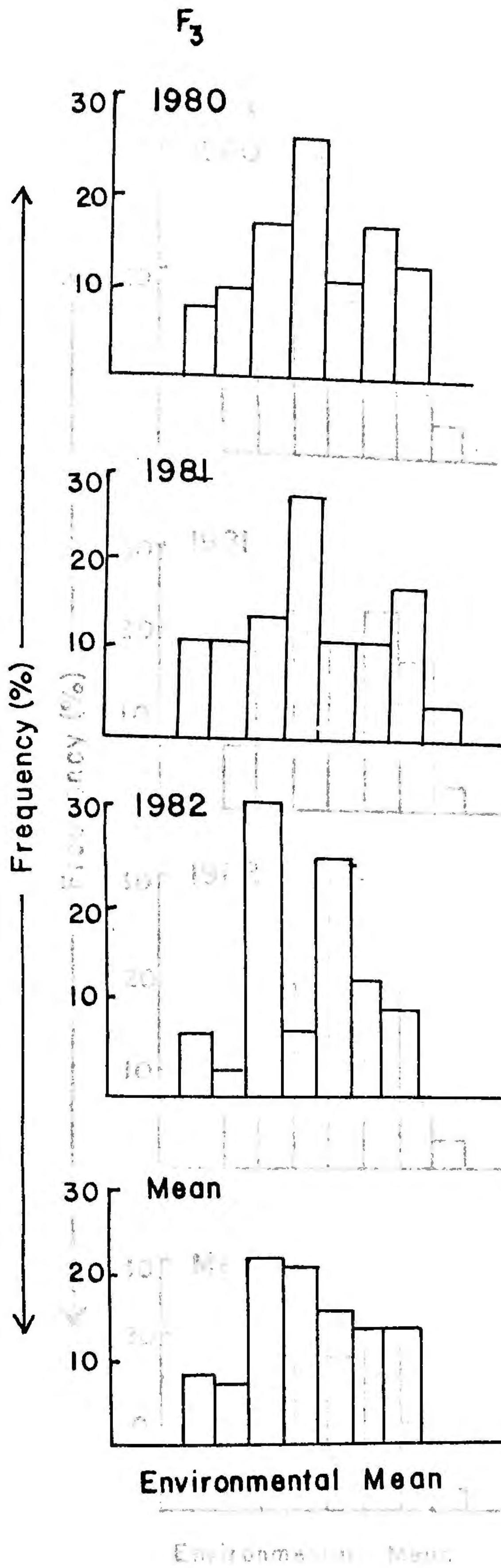
Fig. 12. Distribution of the linear regression coefficients (b_i) among the 30 families of F_3 and F_4 for the Cross 2.

Fig. 13. Distribution of the linear regression coefficients (b_i) among the 30 families of F_3 and F_4 for the Cross 3.

Fig. 14. Distribution of the linear regression coefficients (b_i) among the 30 families of F_3 and F_4 for the Cross 4.

Fig. 15. Distribution of the linear regression coefficients (b_i) among the 30 families of F_3 and F_4 for the Cross 5.

Fig. 16. Distribution of the linear regression coefficients (b_i) among the 30 families of F_3 and F_4 for the Cross 6.



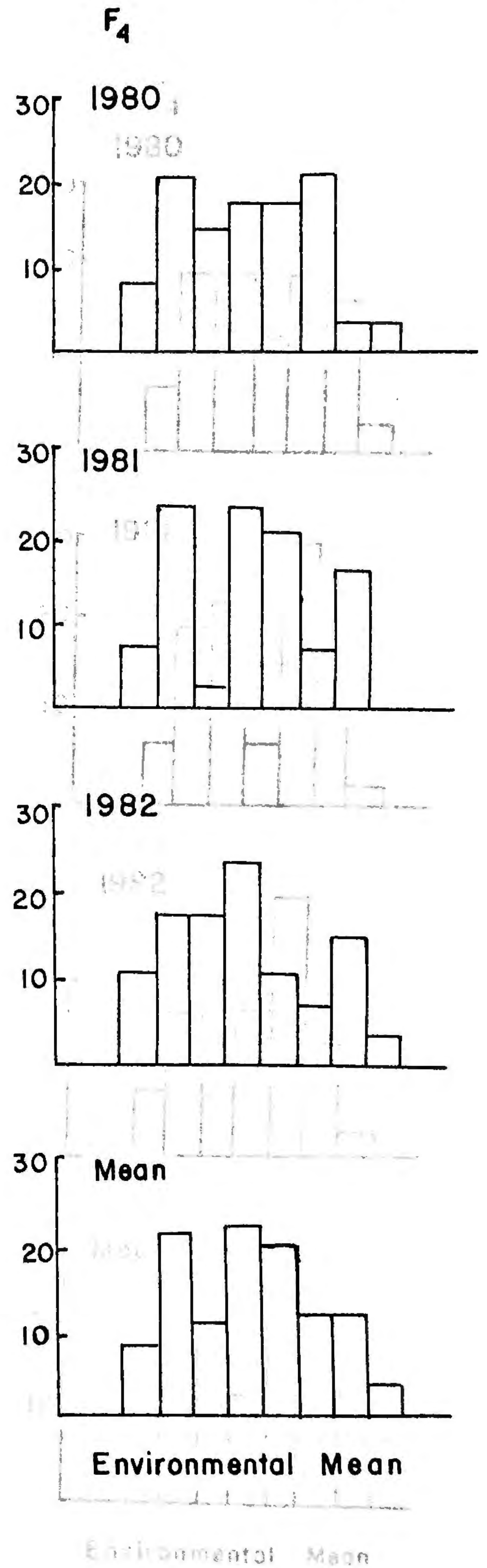
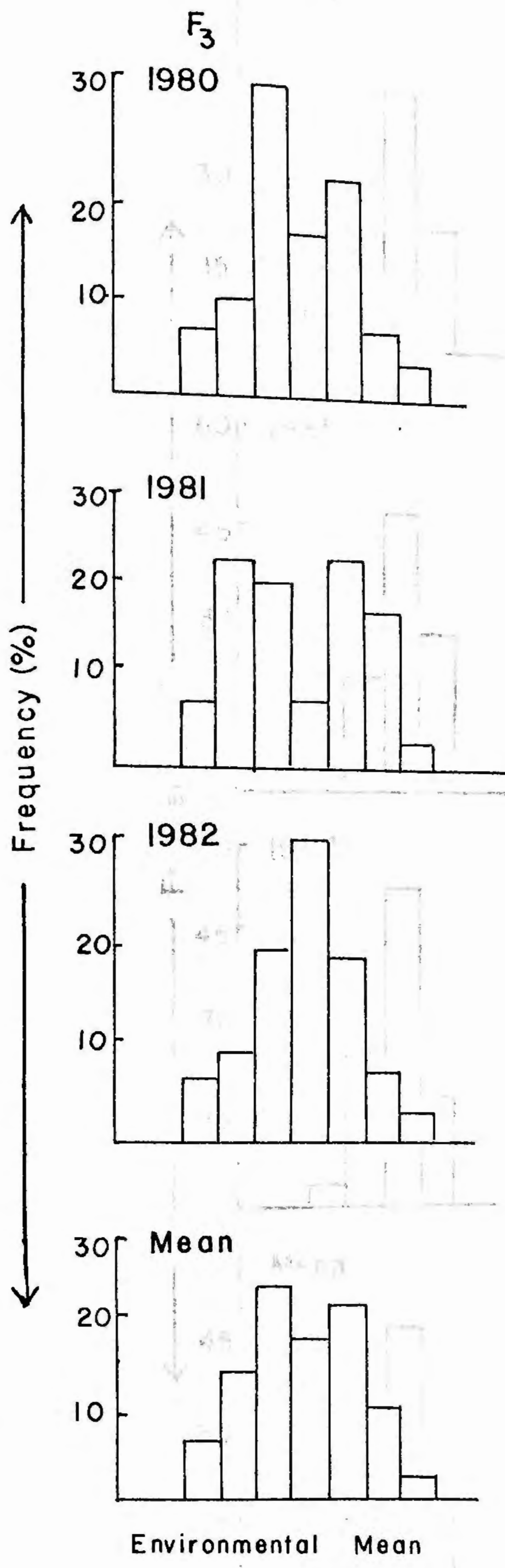


FIG. 11



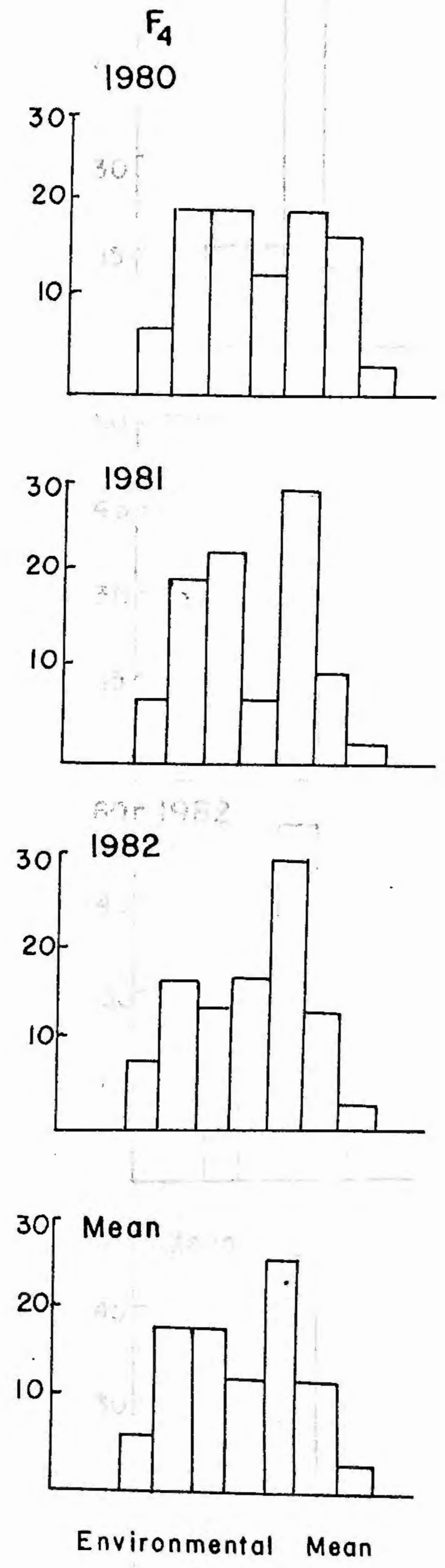
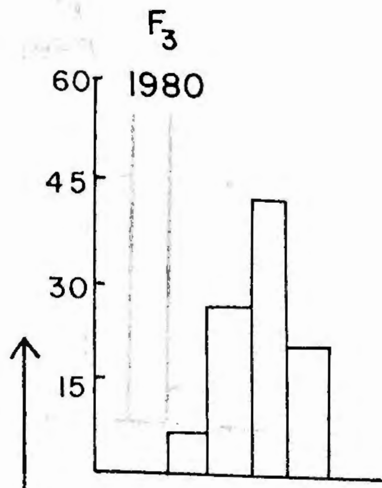
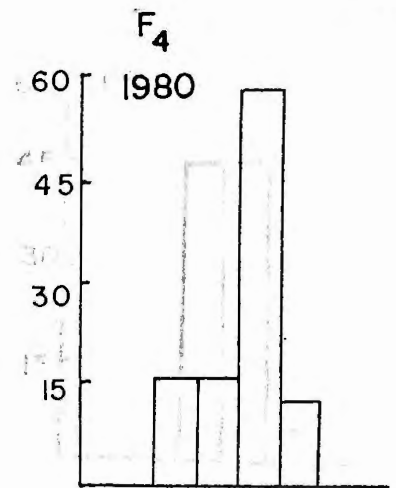


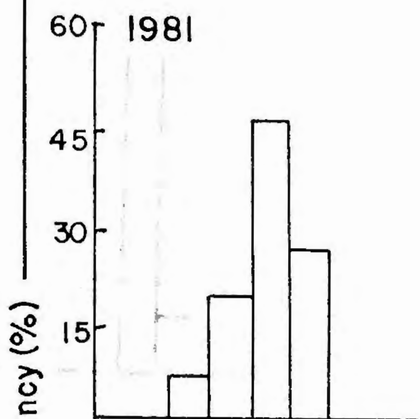
FIG. 12

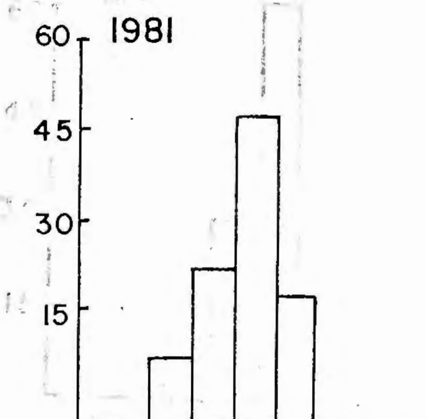
F_3



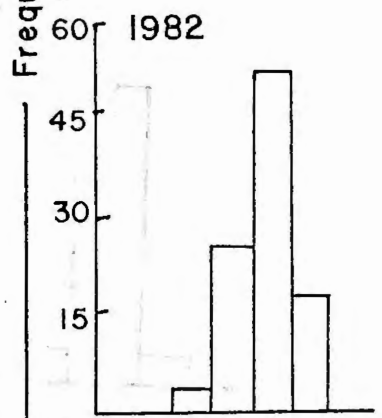
F_4

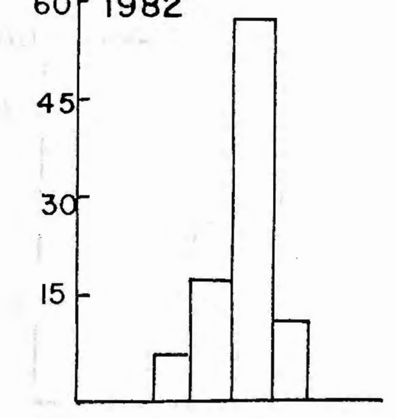


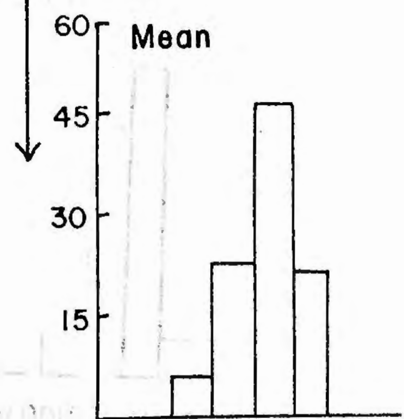


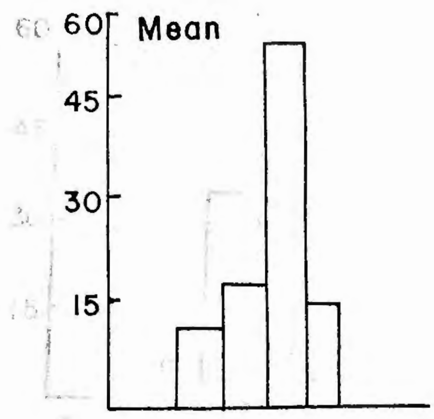


Frequency (%)





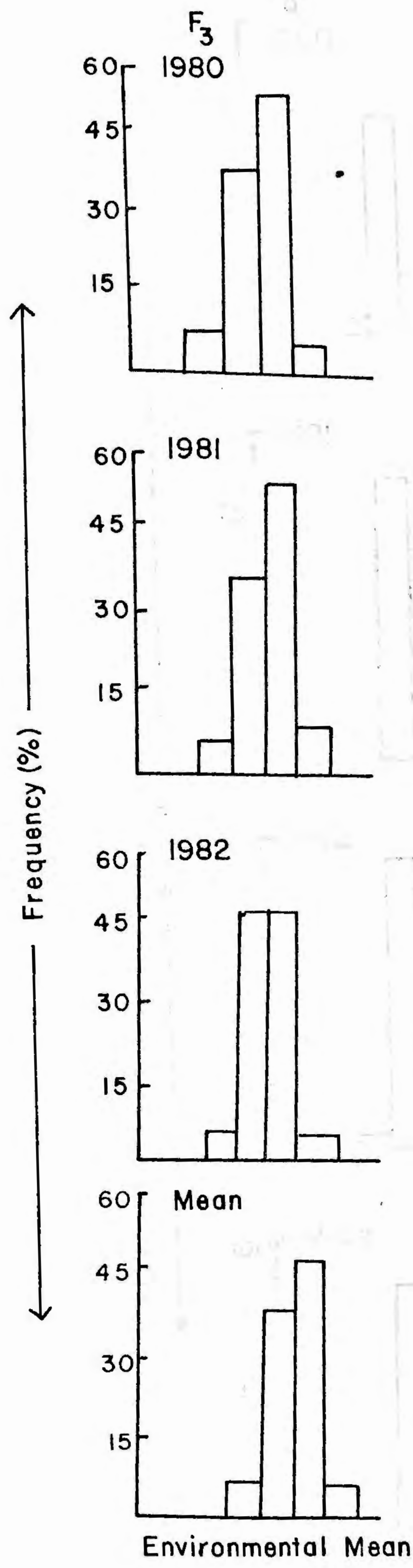




Environmental Mean

Environmental Mean

FIG. 13



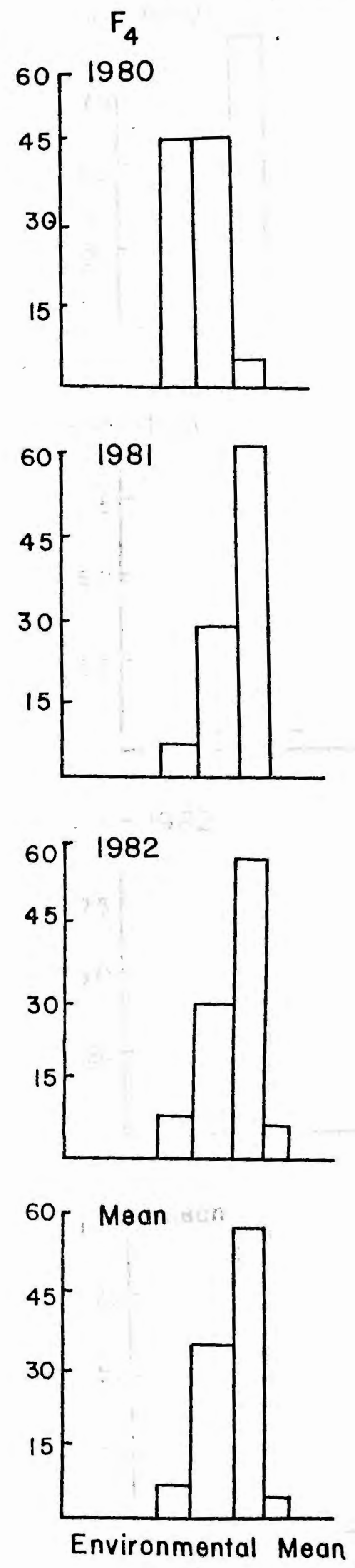


FIG. 14

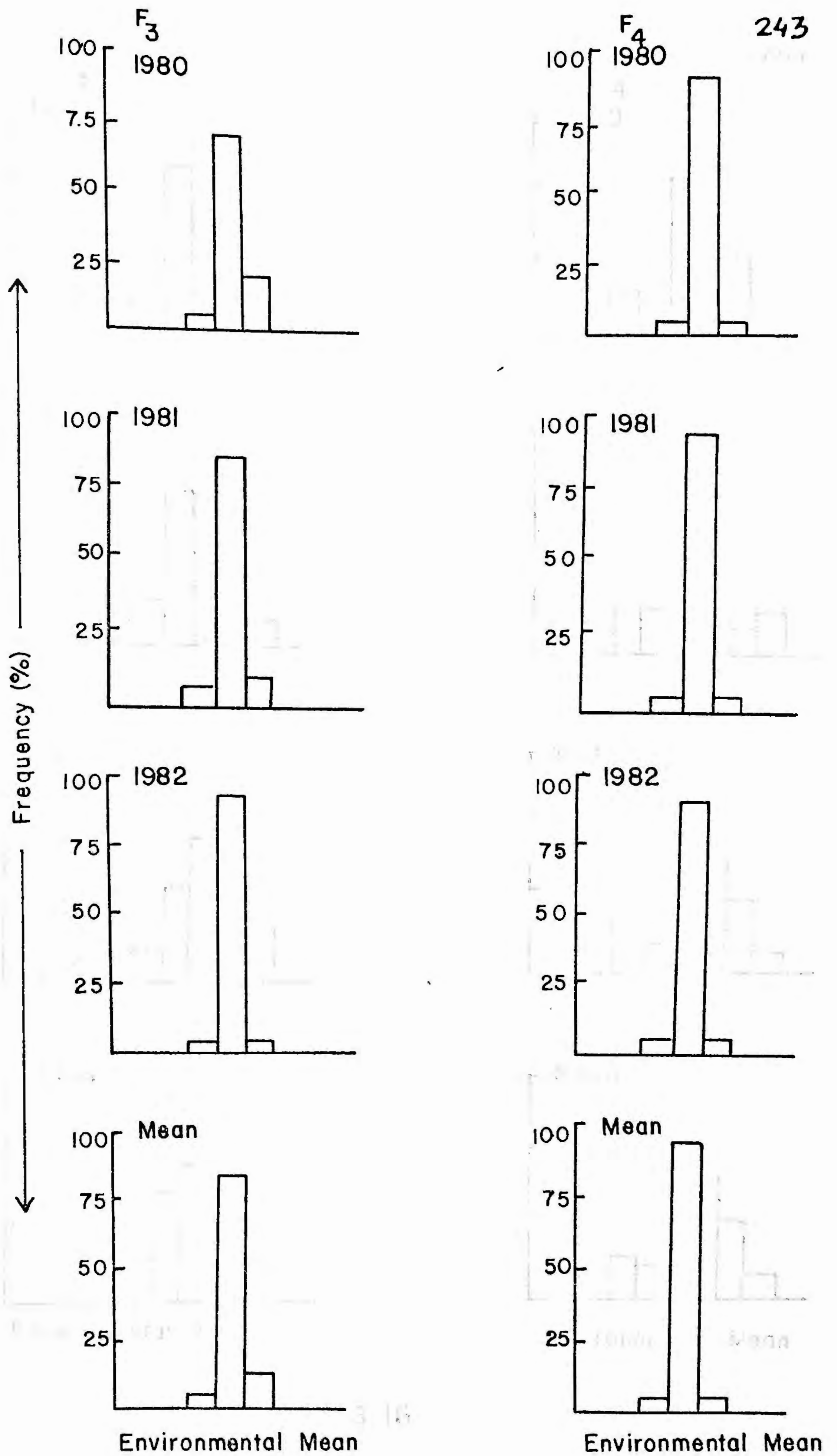


FIG. 15

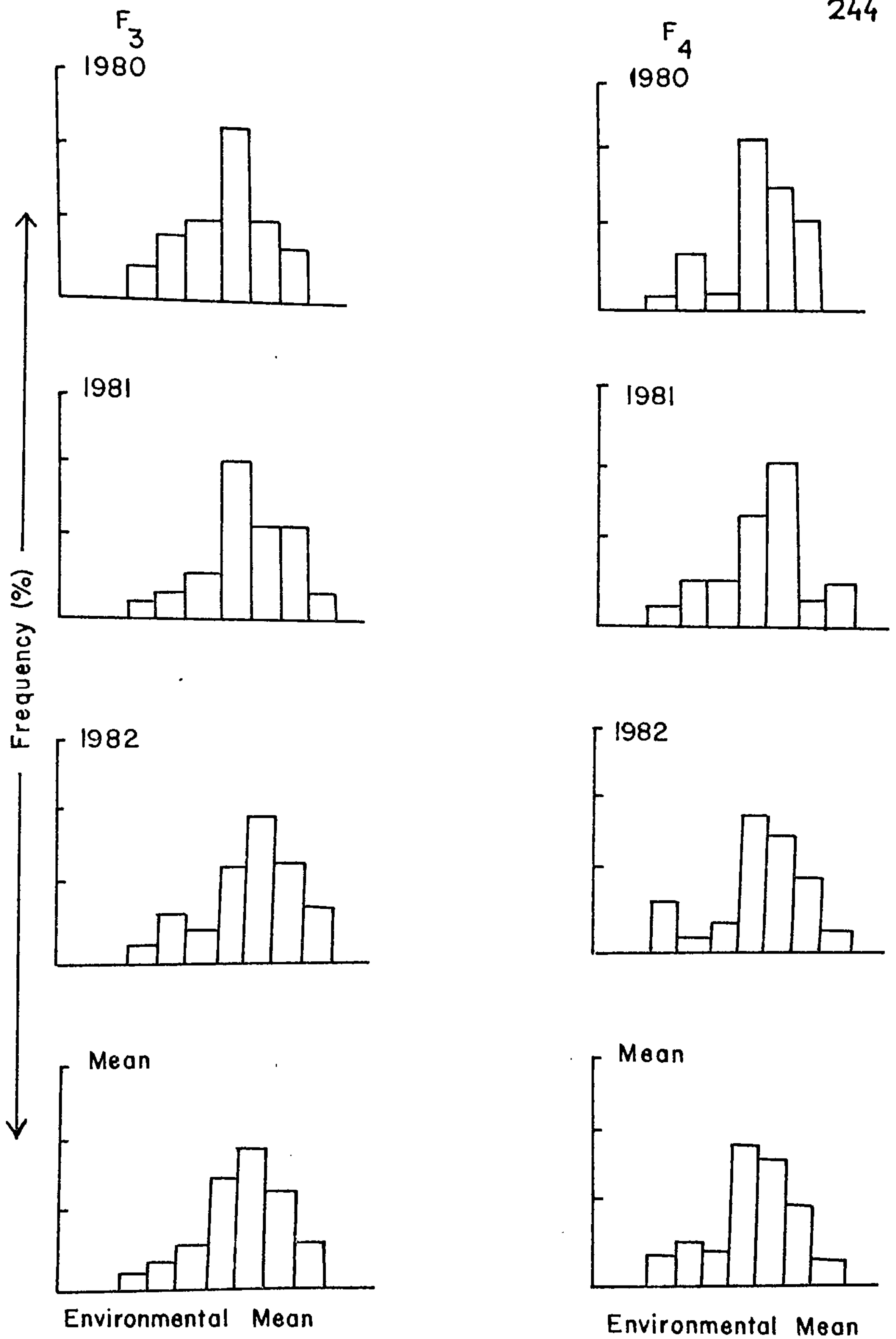


FIG. 16

DISCUSSION

Genotype-environment interaction.

Experiment 1 to 5.

Plant breeders are well aware of the problems posed by the genotype-environment interactions in breeding better genotypes, but until recently, there was no agreement among them about the analytical approaches which could be used to provide reliable estimates of genotype-environment interactions. Two main approaches, one purely statistical (Yates and Cochran, 1938; Finlay and Wilkinson, 1963; Eberhart and Russell, 1966) and the other based on biometrical genetics (Mather and Jones, 1958; Jinks and Stevens, 1959; Bucio Alanis, 1966; Bucio Alanis and Hill, 1966; Perkins and Jinks, 1968a,b; Bucio Alanis et al., 1969) are now available. Both types of analysis have yielded similar results in showing that the genotype-environment interaction component is often a linear function of the environmental means. In the present work a major portion of these interactions both in the parental and progeny generation was accounted for by the linear function of the environmental values although a significant portion was independent of this linear component.

The estimates of the δ^2_g, δ^2_e, δ^2_{gxe} and δ^2_w were derived and found that the main effects and their interaction are highly significant in all the five experiments. The

genotype-environmental interaction component of variation δ^2_{gxe}, was however consistently the greater. It indicates that gxe interaction is one of the major sources of variation shown by coleoptile length. Four different assessment of environments were tested and it was found that the independent environmental assessment is equally good as those of dependent environmental assessment. All the four types of environmental assessment gave very similar results as those often in nicotina rustica (Perkins and Jinks, 1973) though deviations are expected when parents are used as independent z_j estimation.

The adequacy with which the environments are assessed depends upon the degree of relationship between the genotypes whose interactions are to be investigated and the genotypes used to assess the environment, and also upon the purposes for which the genotype-environmental interaction assessments are required. If a mere ranking of the genotypes is required according to the magnitude of their linear regression coefficients, $\bar{\beta}$ + β_d's (when derived from the regression of a genotypic performance in each environment against an environmental assessment), it is only necessary for the joint regression item to be significant when tested against the joint remainder. If however, genetical interpretation of their linear genotype-environmental interactions are to be made, two further criteria must be satisfied (Freeman and Perkins, 1971). The joint remainder should be non-significant when

tested against the variance within genotypes and environments (between individuals) and the joint regression coefficient, $\bar{\beta}$ should not be significantly different from one. In the first five experiments the results of applying these two criteria to the joint regression analyses of the different genotypes against the different kinds of independent environmental assessments shows that independent assessment of the environment satisfies both the criteria. Perkins and Jinks, (1973) and Fripp, (1972) suggested that to obtain stable results from the joint regression when the environmental measure used is the independent variate should be based upon a large number of observations. The results obtained from the significance of the heterogeneity of regression and of the heterogeneity of remainder in the joint regression analyses of the genotypes against the different kinds of environmental assessors (first five experiments), clearly indicated that there are significant linear and non-linear genotype-environment interactions.

The rank correlations (Spearman, 1904) over the 60 inbred lines between the linear regression coefficient, $1 + \beta_d$, obtained with the dependent environmental component, e_j, and the corresponding coefficient, $\bar{\beta} + \beta_d$, obtained with each kind of independent environmental component, z_j, are given in table 40. On the basis of these correlations there is little to choose between the different kinds of environmental

assessment since all are highly significant and all have very high values.

The correlation over the twelve genotypes or 60 inbred lines between the measures of their relative mean performances (the additive genetical component, $[d]$ and their linear sensitivities to macro-environmental differences (the linear interaction coefficient, β_d) were very small and non-significant which suggested that these two aspects of the phenotype are under independent genetical control. These results coincide with the findings of Perkins and Jinks (1968b, 1973) and Paroda and Hays (1971) that both these components are under the control of different genes system in <u>nicotiana rustica</u> and barley respectively.

Rank correlation over the 60 inbred lines for 58 degrees of freedom between the average variance within environments, δ^2_w , and the linear regression coefficient, β_d, and the total variance over environments $\bar{V}_{G+E}$, which are, respectively a measure of sensitivity to micro-environmental variation, of linear sensitivity to macro-environmental differences and of total sensitivity (linear and non-linear) to macro-environmental differences, are given in table 41. The rank correlation between the β_d's and δ^2_w's is significantly negative i.e., the greater the linear sensitivity to environmental differences, the smaller the sensitivity to micro-environmental variation. There is no significant correlation between the rankings of the

total variance over environments, $\bar{V}_{G+E}$, and the average variance within environments, δ^2_w. Perkins and Jinks, (1973) reported a fair degree of independence in the genetical control of sensitivity at the micro and macro-environmental levels.

The estimates of number of effective factors controlling the differences among the 60 lines for the additive genetical component and for the linear regression coefficients indicated that 7 to 8 and 3 to 6 effective factors respectively are operating. Perkins and Jinks (1968b, 1973), Mather and Jinks (1971) and Eaves and Brumpton (1972) reported 1 to 14 effective factors controlling the differences among the lines for the additive genetical components and for the linear regression coefficients.

Diallel cross analysis:

Experiment 6.

Estimates of heritability was moderate to high in all the five temperatures including overall analysis. The narrow sense heritability was very close to broad sense heritability. It implied that the major part of the total phenotypic variations can be attributed to genetic effects. It also indicated that additive and or additive x additive genetic effects contributed more towards higher heritability estimates. The genotype-environment interactions were found to be operative in these diallels but a part of genetic effects were independent of the gxe effects. Supporting evidence for this conclusion was obtained from statistical tests of various genetic parameters. These results are indications of correspondence between genotype and phenotype. It is therefore expected that effective selection should be possible for the character in segregating generations of hybrids among at least certain of the parents tested.

Epistasis was found to be an important feature in 10-parent diallels. Complementary type of gene interactions were noted in a single parent. These interactions were associated with parent 3 (Innia- 66), in five temperatures. Other parents did not show any non-allelic gene interactions. Non-allelic gene interaction increases V_r and decreases W_r values (Allard, 1956). As non-allelic gene interactions were detected in 10-parent diallels the regression coefficients were less

than one and non-significant in most of the temperature environments. Excluding the interacting array significant W_r, V_r regressions were obtained which were almost equal to unity, and the regression line did not deviate from the line of unit slope. A clear grouping of parents in dominance-recessive relationship of the parents on the W_r, V_r graphs were noted along the regression lines. The relationship of the parents were not consistent and varied with the temperature environments.

Examination of the estimated components of variation shows that the dominance components (H_1) were greater than that of additive genetic component (D) for 20°C and 25°C in the 10-parent diallel. But in the excluding analysis H_1 was lower in magnitude than that of D in most of the environments. The ratio $(H_1/D)^{\frac{1}{2}}$ indicated the presence of an overall partial dominance in 10-parent and 9-parent diallel. In the W_r, V_r graphs a partial dominance was noted in 10-parent diallel but in the excluding analysis the graphical results and the components of variation agree with each other. Jinks (1955) in his analysis of diallel crosses noticed a drop in apparent degree of dominance when arrays showing non-allelic interactions were omitted. Allard (1956) also reported that the over dominance shown by the ratio $(H_1/D)^{\frac{1}{2}}$ might be confounded with the complementary type of gene action as it has been detected in 10-parent diallel. Kempthrone (1954) also thinks

that estimate of H may be biased upward by the presence of epistatic variation resulting in a biased estimated for the degree of dominance. Robinson and Comstock (1955) noted that linkage equillibrium resulted in an upward bias of H. They reported that gene pairs entering the cross, in coupling phase gave an upward bias for D, while that in repulsion phase gave a downward value for D. The presence of non-allelic interaction might, therefore, be responsible for the inflated values of H_1 and linkage might have affected D values downward resulting in biased upward estimates for the degree of dominance as indicated by $(H_1/D)^{\frac{1}{2}}$ in the 10-parent diallel.

The probable outcome of selection in specific crosses can be assessed as follows. The diallel analysis indicated that near top dominant and near bottom recessive genotypes were present among the 10-parents. Thus, so far as genes displaying dominance are concerned, the units of selection have already been reached, or nearly so. Progress under selection must, therefore, depend largely on a system of numerous minor genes that do not display dominance. The diallel analysis indicates that these non-dominance genes control a relatively significant part of the total genetic variability. It also indicates that epistasis is a common feature of the system. It appears that the rate of progress under selection will be encouraging.

The diallel cross analysis gives an indication that polygenes with plus and minus effects are more or less equally

distributed among the 10-parents. If that is the case, inter crossing among selected lines derived from different hybrids should provide opportunity for progress beyond that offered by the hybrid between any single pair of parents. The present diallel cross analysis gave sufficient idea of the probable outcome of selection of these polygenes, and the non-allelic gene interactions indicate that immediate effect of selection between and within lines will be possible.

The diallel study indicated that genotype-environment interaction was a common feature. Both additive (D) and dominance (H_1) genetic variation were found to interact with the temperatures. The epistatic effects also showed significant interaction with temperatures. Jinks and Mather (1955), Jinks and Stevens (1959), Bucio Alanis and Hill (1966), Bucio Alanis, Perkins and Jinks (1969), Jinks and Perkins (1969) and Breese (1969) studied the relative sensitivity of additive, dominance and epistatic components and found situations in which dominance components were more sensitive or equally sensitive than additive components.

It is concluded that high heritability, complementary gene interaction, dominant and recessive gene effects suggested that these parents could be used to develop better lines, and that selection programmes will be effective in early generations. Significant gxe interaction effects indicated that trial in different temperatures must be made during selection breeding programme.

Single cross analysis:

Experiment 7.

Joint scaling text (χ^2) of Cavalli (1952) based on 3-parameter estimate indicated that non-allelic gene interaction was a part of the genetic system that controls the mean expression of different generations of the crosses studied. Chi-square based on 6-parameter estimate was significant in few crosses only. In those cases trigenic or linked digenic epistasis might be involved (Hill, 1966).

The estimates of the 6-parameter for the various gene effects showed that additive and dominant gene effect made a major contribution to variation in most of the crosses. The sign of d estimate is not important as it depends on $\bar{P}_1$ and $\bar{P}_2$ ($d = \frac{1}{2}\ \bar{P}_1 - \bar{P}_2$). The dominant gene effects were positive in all the eight crosses indicating the importance of positive dominant genes in the inheritance of the character. The absolute magnitude of h effects were smaller than that of the d effect in some of the crosses. It indicated that the d effect contributed more to the inheritance of the character. The effects of temperature on the expression of d and h effects were highly significant in all the eight crosses. Allard (1956) reported that additive and dominance effects of gene might be considerably modified by the environmental changes. Moreover, the standard error attached with the h effect was high which was due to the differential effects of

environments on the gene responsible for the dominance expression. Robinson and Comstock (1955) thought that genotype-environment interaction would increase the standard error of h estimate.

With regard to the individual epistatic effects, the absolute magnitude of i effect was less than that of j and l effects in most of the crosses. The additive x dominance and dominance x dominance gene effects were also significant in majority of the crosses. It indicated that the inheritance of the character was not simple and straightforward. Highly significant temperature effects on the expression of epistatic gene action were noted in all the crosses.

The D and H estimates of components of variation were considerable in magnitude in all the eight crosses studied. The D and H estimate was significant in all the crosses. It indicated that both dominance and additivity played an important role in the inheritance of the character but the former was greater than that of the latter, Krishnaswami _et al_. (1964) and Sengupta _et al_. (1974) found that dominance was more important than additive variation.

Dominance relationship as measured by potence ratio method was found to be similar in the F_1, F_2, F_3 and F_4 generations in most of the crosses whereas in a few crosses the degrees of dominance in the F_1 generation and in the F_2,

F_3 and F_4 generations were dissimilar. This dissimilar expression of dominance was due to the confounding effects of the epistasis gene action for which the h_2, h_3 and h_4 values were either lower or higher than that of the corresponding h_1 values. Similar situation was met in a number of crop plants (Paul et al. 1976; Singh and Gupta, 1969; Paroda and Joshi, 1970a, b; Tandon et al., 1970). Dominance relationship as measured by $(H/D)^{\frac{1}{2}}$ showed partial dominance to complete dominance in these crosses.

An effective factor has been described by Mather (1949) as the smallest unit of hereditary material that is capable of being recognised by the method of biometrical genetics. It may be a closely linked gene, or at the lower limit a single gene. The number of effective factors were calculated by the following four different methods of estimation as developed by Castle and Wright, 1921; Mather, 1949; and Burton, 1951. The estimate K_1 is based on certain assumptions (i) all genes are equally important; (ii) one parent has all the minus genes and the other parent has all the plus genes; (iii) no linkage exists between parental genes; (iv) gene effects combined additivity; (v) degree of dominance for all the plus genes is similar and (vi) no interaction exists between pertinent non-allelic genes. Failure of one of these assumptions listed above to be fulfilled in the parents will under estimate the number of effective factors. That the K_1 estimates were low

in all the crosses was due to the fulfilment of the assumption listed in this paragraph. The K_2 estimates, however, gave 3 to 7 effective factors in different crosses. It indicated that K_2 provided better estimates than K_1. The K_2 estimate remain unaffected in cases where the plus and the minus genes in the parents were not iso-directionally distributed (Mather, 1949).

Broad sense heritability was high in all the crosses. It indicated that a major part of the total phenotypic variation was genetic in nature. Narrow sense heritability was also high in all the crosses and suggested that most of the genetic variations were of additive x additive in nature.

Parent dependent genotype-environment interaction:

Experiment 8.

Eberhart and Russel (1966) defined both the linear (b_i) and non-linear ($\bar{S}^2_d$) functions of the genotype-environment interaction as "stability parameters" β_i (Linear regression) and $\bar{S}^2_d$ (deviation from the regression) respectively. They emphasized that the phenotypic expression (Y) of a particular genotype (i) in a specific environment (j) depends on the mean expression (μ_i), the linearity of response of the genotype to change in the environment (β_i) and the extent of residual deviations from the regression (δ_{ij}). Perkins and Jinks (1968b) observed that these two components of the genotype-environmental interactions are independent and presumably subject to the control of different genetic systems. In the present material significant regression items as well as heterogeneity of regression indicates that b_i and $\bar{S}^2_d$ is under genetic control.

The non-significant correlation between mean, b_i and $\bar{S}^2_d$ was obtained in all generations. Busch et al. (1976) reported a non-significant association between mean and $\bar{S}^2_d$ whereas Joarder et al. (1978) found significant association between mean and $\bar{S}^2_d$. A positive correlation between mean performance and linear (b_i) sensitivity has been found in a number of previous studies (Eberhart and Russel, 1966; Perkins and Jinks,

1968a,b); Westerman, 1971; Busch *et al.*, 1976; Joarder *et al.*, 1980a,b). It is therefore indicated that unlike other reports prediction about linear response as well as stability in different environments of either parents or of segregating generations would not be possible on the basis of their mean performence (Jinks and Mather, 1955; Perkins and Jinks, 1968a, b; Paroda and Hayes, 1971; Joarder *et al.*, 1978).

Previous investigations of pure breeding lines and their F_1's (Perkins and Jinks, 1968a and b; Perkins, 1970; Paroda and Hayes, 1971; Joarder and Eunus, 1977) and in one instance the F_2 and first backcross generations (Bucio Alanis *et al.*, 1969 and Joarder *et al.*, 1978) have shown that mean performance and linear (b_i) and non-linear ($\bar{S}^2_d$) sensitivity to the environment are controlled at least in part by different genetical systems and that mean performance and linear (b_i) sensitivity can be successfully predicted from one generation to another of the same cross. The present investigation has extended these findings to the F_3 and F_4 generations of six crosses which were chosen to contrast in their performance and in their linear (b_i) and non-linear ($\bar{S}^2_d$) sensitivities.

The components d_i, b_i and $\bar{S}^2_d$ in the F_2, F_3 and F_4 generations as summarized in the result leave no doubt that the differences in coleoptile length and in linear (b_i) and non-linear ($\bar{S}^2_d$) environmental sensitivities among the six parents is consistantly reflected in the properties of the

advanced generations of the six crosses among them. It is also apparent that the non-significant correlation between mean performance and linear (b_i) as well as non-linear ($\bar{S}^2_d$) sensivivity shown by the parental lines is also consistantly maintained in the advanced generations. A very similar result has been reported by Bains (1976) in wheat yield.

A clear evidence of segregation for differences in linear (b_i) sensitivity among the F_3 and F_4 families from the crosses where parents differ in respect of linear (b_i) sensitivity (cross 1 and 2) whereas little evidence of segregation for differences in linear (b_i) sensitivity among the F_3 and F_4 families where both parents of the cross had either a high or a low sensitivity to the environment (crosses 3, 4 and 5). This has been clearly demonstrated in figures 11-16. Furthermore this segregation is symmetrical around a mean value that corresponds with the mean of the parents of each cross. A very similar result was found in wheat yield as reported by Bains (1976). In cross 6, though both parents had a high linear (b_i) sensitivity to the environment, evidence of recombinations of genes controlling the linear (b_i) sensitivity was clear (Fig. 16). It implies that though both the parents of cross 6 (Mexipak- 65 x Penkty) possesses similar linear (b_i) sensitivity to the environment, the genes determining this character was essentially different. For this a wide range of b_i values were found among the F_3 and F_4 families of cross 6.

As regards non-linear ($\bar{S}^2_d$) sensitivity there was no clear cut pattern of segregation in advanced generations as was found in the case of b_i values. But it is clear that this character is under genetic control and inheritance pattern is not simple and straight forward. Busch et al. (1976) reported that $\bar{S}^2_d$ are inherited simply while Patanothai and Atkins (1974); Eberhart and Russel (1966); Joarder and Eunus (1977) and Joarder et al. (1978) reported that the inheritance of deviations from regression was largely non-additive.

The present study clearly demonstrates that the linear (b_i) and non-linear ($\bar{S}^2_d$) components are subject to genetical control and are subject to the different genetic systems. Perkins and Jinks (1968a,b); Bucio Alanis et al.(1969); Paroda and Hayes (1971); Joarder and Eunus (1977) and Joarder et al. (1978) observed in different crop plants that both linear (b_i) and non-linear ($\bar{S}^2_d$) components are under genetic control and are at least in part subject to different genetic systems. These authors showed that it was possible to accurately predict the linear (b_i) function of advanced generation of a cross between pairs of pure breeding lines from those observed in the parental and F_1 generations. In the present investigation the relative performance and relative linear (b_i) and non-linear ($\bar{S}^2_d$) sensitivities to the environment as well as in their patterns of segregations for sensitivity, the properties of the advanced generations of the six crosses were expected from the corresponding properties of their parents. All aspects are

clearly under genetic control and can, therefore, be selected for crosses initiated from appropriately chosen parents.

This analysis as carried out, illustrates the power of the analytical techniques now available for the use of breeders. As data from a range of environments can be considered as a simple unit, a pattern of genotype-environment interaction is becoming apparent, which will greatly simplify the task of breeders in developing either specific or generally adapted genotypes. As genotype-environment interaction is under genetic control, breeders would be able to select suitable genotypes in advanced generations by growing them under different environmental conditions.

SUMMARY

Genotype-environment interaction for coleoptile length was studied in five separate experiments. The environments used were different temperatures and different nutritional mediums. Genotype-environment interaction was found to be operative and detected in all the experiments. A significant part of the variation was however, independent of the genotype-environment interaction effects.

Both linear and non-linear type of genotype x environment interactions were detected and found to be controlled by different gene systems.

In addition to the usual dependent assessment of the environments, these experiments provided three sources of independent assessment, namely, replicate samples of individual of each genotype, replicate samples of inbred lines and the parental varieties. As far the significance of the heterogeneity of regression and remainder items in the joint regression analysis and the ranking of the genotypes on the basis of their linear regression coefficients are concerned, it made no differences whether the dependent or any one of the three independent measures of the environmental values was used.

The correlation over genotypes between mean performance and linear sensitivity was low and non-significant and the number of effective factors of the largely independent

genetical systems controlling two aspects of phenotype have been estimated to be 3 to 8.

Diallel cross:

Genotype-environment interaction shown by coleoptile length of wheat *Triticum aestivum* L. em Thell, was studied in 10-parent diallel over five different temperature environments. Results showed that the character studied was polygenically controlled and both additive and dominance components of genetic variations were important in the inheritance of these characters. The contribution of additive gene effects were greater compared to that of dominance gene effects.

The total phenotypic variance was found to be almost entirely due to genetic effect and the heritability estimates were noted to be high in all the five temperature environments.

Hyman's analysis of variance indicated that item a and item b were consistently significant in all the temperature environments. Among the b items b_1, b_2 and b_3 were also significant in all the five temperature environments.

The 10-parent diallel showed significant non-allelic interactions whereas analysis excluding the interacting analysis gave significant regression which did not deviate from unity. The distribution of array points in the W_r, V_r graphs showed three distinct groupings in most of the environments showing

most dominant, less dominant and recessive parents.

Non allelic gene interaction detected by W_r, V_r graphs were of complementary type.

On an average the degree of dominance was partial in 10-parent diallel and partial or complete dominance in analysis excluding interacting array.

Interaction between the additive component and the environment was greater than that of the dominance component in the different environments.

<u>Single cross:</u>

Cavalli's (1952) joint scaling test detected non allelic gene interaction in all the environments.

High heritability estimate, indicated most of the phenotypic variations were genetic in nature. Narrow sense heritability estimates were also high indicating importance of additive gene effects in the inheritance of the character.

Non-isodirectional distribution of polygenes resulted in the estimation of a single effective factor when calculated as n_1, n_2 and K_1 whereas, K_2 estimates indicated that 3 to 7 effective factors were involved in controlling the character over different environments.

Both additive (d) and dominance (h) gene effects contributed to the inheritance of the character but the contribution of the latter was much greater in most of the crosses.

Absolute magnitude of epistatic effect (i, j and l) was less than the mean effect (m). In some crosses additive x additive (i) and dominance x dominance (l) and additive x dominance (j) of all the three interaction components occured significantly in addition to d and h effects.

Significant χ^2 values obtained under analysis as per 6-parameter model suggested a complex inheritance pattern in few crosses, not accountable in this type of investigation.

Potence ratio indicated partial dominance to over dominance in different crosses, Dominance ratio indicated partial dominance in majority of the crosses and complete or over dominance in few crosses.

Estimates of D were significant in all the eight crosses whereas the estimates of H in cross 6 were non significant.

Genotype-environment interaction was found to play an important role in the expression of both additive and dominance genes.

Parent dependent genotype-environment interaction:

An investigation of genotype-environment interactions for coleoptile length of six parental and F_2, F_3 and F_4 generations of Triticum aestivum L. em Thell. showed that genotype-environment interactions were operative in parental, F_2, F_3 and F_4 generations and a major portion of these interactions in all the generations (parental, F_2, F_3 and F_4 generations) was accounted for by the linear function of the environmental mean although a significant portion was independent of this linear component. Significant regression items as well as heterogeneity of regression indicate that linear (b_i) and non-linear ($\bar{S}^2_d$) components were under the control of different genetic system.

The non-significant correlation between mean, stability (b_i) and response ($\bar{S}^2_d$) was obtained in all the generations. The components d_i, b_i and $\bar{S}^2_d$ in the F_2,F_3 and F_4 generations indicate that the differences in coleoptile length and in linear (b_i) and non-linear ($\bar{S}^2_d$) environmental sensitivities among the six parents is consistantly reflected in the properties of the advanced generations of the six crosses among them.

A clear evidence of segregation for differences in linear (b_i) sensitivities among the F_3 and F_4 families from the crosses where parents differ in respect of linear sensitivity (cross 1 and 2) whereas there was little evidence of

segregation for differences in linear (b_i) sensitivity among the F_3 and F_4 families where both parents of the cross had either a 'high' or a 'low' sensitivity to the environment (cross 3, 4 and 5). Moreover, these segregations were symmetrical around a mean value that corresponds with the mean of the parents of each cross. In cross 6 though both parents had a 'high' linear (b_i) sensitivity to the environment an evidence of recombinations of genes controlling the linear (b_i) sensitivity was found. It indicates that though both the parents of cross 6 (Mexipak - 65 x penkty) possess similar linear sensitivity to the environment, the genes determining this character were essentially different.

Regarding non-linear ($\bar{S}^2_d$) sensitivity no clear cut pattern of segregation was found though it was present in the case of b_i values. But this character is under genetic control.

REFERENCES

Agrawal, R.K., R. Sharma, G.S. Sharma, R.B. Singh and R. Nandan. 1976. Variability and associations of coleoptile length and other traits in wheat. Indian J. Agric. sci., 47: 234-236.

Allard, R.W. 1956a. The analysis of genetic environmental interactions by means of diallel crosses. Genetics, 41: 305-318.

Allard, R.W. 1956b. Estimation of prepotency from linear bean diallel cross data. Agron. J. 48:537-543.

Allard, R.W. 1956c. Biometrical approach to plant breeding. Brookhaven Symp. Biol. 9: 69-88.

Allard, R.W. 1960. Principles of plant breeding. John Wiley and Sons. Inc. N.Y.

Allan, R.E., O.A. Vogel, and J.R. Burleigh. 1962. The effect of temperature on coleoptile elongation of three groups of wheat varieties. Wheat Inform. Serv. Kyoto. 14: 12-14.

Allan, R.E., and O.A. Vogel, 1964. F_2 monosomic analysis of coleoptile and first-leaf development in two series of wheat crosses. Crop. Sci. 4: 338-339.

Anderson, V.L. 1953. Ph.D. thesis, Iowa State College Library (cited by Hayman, B.I. 1955. The description and analysis of gene action and interaction. Cold spring Harbor Symposia on quantitative Biology. Vol. XX.)

Anderson, V.L. and O. Kempthorne, 1954. A model for the study of quantitative inheritance. Genetics, 39: 883-898.

Baker, R.J., 1969. Genotype-environment interaction in yield of wheat. Can. J. Plant Sci., 40: 743-751.

Bains, K.S., S.C. Anand and H.S. Anlakh, 1973. Inheritance of coleoptile size in bread wheat. The J. of Heredity, 64: 340-42.

Bains, K.S., 1976. Parent dependent genotype-environment interaction in crosses of spring wheat. Heredity, 36: 163-171.

Bhatt, G.M., 1972. Inheritance of heading date, plant height and Kernel weight in two spring wheat crosses. Crop Sci., 12: 95-98.

Bhatt, G.M., and C.O. Qualset, 1975. Genotype-environment interaction in wheat: Effects of temperature on coleoptile length. University of Sydney, Plant Breeding Institute, Narrabri, N.S.W. Australia. Experimental Agriculture 12: 17-22.

Breese, E.L., 1969. The measurement and significance of genotype-environment interaction in grasses. Heredity, 24: 27-44.

Briggle, L.W., 1963. Heterosis in wheat. A review crop sci., 3: 407-412.

Briggle, L.W., E.L. Cox, and R.M. Hays, 1967. Preference of a spring wheat hybrid, F_2, F_3 and parent varieties of five population levels. Crop Sci., 71:465-470.

Brown, L.R., 1963. Man, Land, and Food; looking ahead at World Food Needs. Foreign Agr. Econ. Rept. No. 11, Economic Research Service, U.S. Dept. of Agr. 153 pp. illus.

Bucio-Alanis, L. 1966. Environmental and genotype-environmental components of variability. I. Inbred lines. Heredity, 21: 387-397.

Bucio-Alanis, L. and J. Hill, 1966. Environmental and genotype-environmental components of variability. II. Heterozygotes. Heredity, 21: 399-405.

Bucio-Alanis, L., J.M. Perkins and J.L. Jinks. 1969. Environmental and genotype-environmental components of variability. V. segregating generations. Heredity 24: 115-127.

Burleigh, J.R., R.E. Allen, and O.A. Vogel. 1964. Varietal differences in seedling emergence of winter wheats as influenced by temperature and depth of plants. Agron. J. 57: 195-198.

Burleigh, J.R., R.E. Allan and O.A. Vogel. 1964. Effect of temperature on coleoptile elongation in eight wheat varieties and selections. Agron. J. 56: 523-524.

Burton, G.W., 1951. Quantitative inheritance in pearl milled, (Pennisetum glaucum). Agron. J., 43: 409-417.

Busch, R.H., J. Hammond, and R.C. Frohberg, 1976. Stability and performance of hard red spring wheat bulks for grain yield. Crop. Sci. 16: 256-259.

Castle, W.E. and S.A. Wright, 1921. An improved method of estimating the number of blending inheritance. Science, 54: 223.

Cavalli, L.L. 1952. An analysis of linkage in quantitative inheritance. Quantitative Inheritance, H.M.S.O., London, pp. 135-144.

Chowdhry, A.R. and R.E. Allan. 1963. Inheritance of coleoptile length and seedling height and their relation to plant height of four winter wheat crosses. Crop Sci. 3: 53-8.

Clerk, J.A., 1936: Improvement in wheat. Yearbook of Agriculture, 1936. U.S. Department of Agriculture, Washington, D.C. pp. 207-302.

Connolly. V., and G. Simchen. 1968. Linkage to the incompatibility factors and maintenance of genetic variation in selection lines of <u>Schizophyllum commune</u>. Heredity, 23: 387-402.

Crumpacker, D.W. and R.W. Allard, 1962. A diallel analysis of heading date in wheat Hilgardia, 32: 275-318.

Curnow, R.N. 1963. Sampling the diallel cross. Biometrics, 19: 287-306.

Eaves, L.J. and R.J. Brumpton. 1972. Factors of Covariation in <u>Nicotina rustica</u>. Heredity, 29: 151-175.

Eberhart, S.A. and W.A. Russell. 1966. Stability parameters for comparing varieties. Coop. Sci., 6: 36-40.

Fick, G.N., and C.O. Qualset, 1976. Seedling emergence, coleoptile length and plant height relationship in crosses of dwarf and standard height wheats. Euphytica, 25: 679-84.

Fisher, R.A. 1918. The correlation between relative on the supposition of Mendalian inheritance. Trans. Roy. Sec. Edin. 52: 399-433.

Fisher, R.A., F.R. Immer and O. Tendin, 1932. The genetical interpretation of statistics of third degree in the study of quantitative inheritance. Genetics, 17: 107-124.

Fisher, R.A., 1946. Statistical methods for research of Worker. 10th Edn. Oliver and Boyd, Edinbourgh.

Finlay, K.W. and G.N. Wilkinson, 1963. The analysis of adaptation on plant breeding programme. Aust. J. Agric. Res., 14: 742-754.

Freeman, G.H. and J.M. Perkins, 1971. Environmental and genotype environmental components of variability. VIII. Relations between genotypes grown in different environments and measures these environments. Heredity, 27: 15-23.

Fripp, Y.J., and C.E. Caten, 1971. Genotype-environmental interactions in Schizophyllum commune. 1. Analysis and character. Heredity, 27: 393-408.

Fripp, Y.J., 1972. Genotype-environmental interaction in Schizophyllum commune. II. Assessing the environment. Heredity 28: 223-238.

Fripp, Y.J., and C.E. Caten, 1973. Genotype-environmental interaction in Schizophyllum commune. III. The relationship between mean expression and sensitivity to change in environments. Heredity 30: 341-349.

Fyfe, J.L. and N. Gilbert. 1963. Partial diallel crosses. Biometrics, 19: 278-286.

Gardner, C.O. and S.A. Eberhart, 1966. Analysis and interpretation of the variety cross diallel and related population. Biometrics, 22: 439-452.

Gilbert, N.E. G. 1958. Diallel cross in plant breeding. Heredity, 12: 477-492.

Gill, K.S., G.S. Bhullar and G.S. Mahal, 1979. Gene action in seven parent diallel cross of macaroni wheat. Indian J. agric. sci., 49: 827-831.

Gill, K.S., G.S. Nanda, Gurdar Singh and K.L. Sehgal, 1979. Inheritance of grain number, grain size, protein content and grain yield into spring x winter wheat crosses. SABRAO Journal, 11: 1-7.

Gill, K.S., G.S. Bhullar, K.S. Bains and Alok Bhatia, 1981. Combining ability for coleoptile length in bread wheat. Indian J. Genet. 41: 37-40.

Griffing, B. 1950. Analysis of quantitative gene action by constant parent regression and related techniques. genetics, 35: 303-321.

Griffing, B. 1956a. A generalised treatment of diallel crosses in quantitative inheritance. Heredity, 10: 31-50.

Griffing, B. 1956b. Concept of general and specific combining ability in relation to diallel crossing systems. Aust. J. Biol. Sci., 9: 463-493.

Hayman, B.I. 1954a. The analysis of variance of diallel table. Biometrics, 10: 235-244.

Hayman, B.I. 1954b. The theory and analysis of diallel crosses. Genetics, 39: 789-809.

Hayman, B.I. 1957. Interaction, heterosis and diallel crosses. Genetics, 42: 336-355.

Hayman, B.I. 1958. The theory and analysis of diallel Cross. II. Genetics, 43: 63-85.

Hayman, B.I. 1958. The separation of epistasis from additive and dominance variation in generations means. Heredity, 12: 371-390.

Hayman, B.I. 1960. The theory and analysis of diallel crosses. III. Genetics, 45: 155-172.

Hayman, B.I. 1960. Heterosis and quantitative inheritance. Heredity, 15: 324-327.

Henderson, C.R. 1948. Estimation of general, specific, and maternal combining abilities in crosses among inbred line of swine. Unpublished Ph.D. Dissertation. (Iows State College Library, Ames., Iows).

Henderson, C.R. 1952. Specific and general combining ability in 'Heterosis' (Ed. J.W. Gowon) Iows State College Press: Ames.

Hill, J., Recurrent backcrossing in the study of quantitative inheritance. Heredity 21: 85-120.

Hinkelmenn, K. and O. Kempthorne, 1963. Two classes of group divisible partial diallel crosses. Biometrika 50: 281-291.

Horner, T.W., R.E. Comstock, and H.F. Robinson, 1955. Non-allelic gene interaction and the interpretation of quantitative genetic data. North Carolina Agri. Exp. Station, Bull. No. 118.

Hsu, P. and P. D. Walton, 1970a. The quantitative inheritance of morphological and agronomical characters in spring wheat. Euphytica, 19: 54-60.

Hsu, P. and P.D. Walton, 1970b. The use of factor analysis in determining characters for yield selection in wheat. Can. J. Genet.; 12: 738-742.

Hull, F.H. 1945. Regression analysis of yield of hybrid corns and inbred parent lines. Maize Genetic Newsletter 19: 21-27.

Hunt, O.J. and D.G. Miller, 1964. Coleoptile length, seed size, and Emergence in Intermediate Wheatgrass (Agropyron intermedium (Host) Beauv.) Wyoming Agr. Exp. Sta., as Journal paper No. 237.

Jatasra, D.S. and R.S. Paroda, 1978a. Use of F_2 generations for combining ability in wheat. Cereal Research Communications, 6: 265-271.

Jatasra, D.S. and R.S. Paroda, 1978b. Genetic divergence in wheat under different environmental conditions. Cereal Research Communications, 6: 307-317.

Jatasra D.S. and R.S. Paroda, 1979a. An 8x8 diallel analysis for plant height in bread wheat. Indian J. agric. Sci., 49: 909-914.

Jatasra, D.S. and R.S. Paroda, 1980a. Genetic architecture of ear emergence in wheat. Haryana agric. Univ. J. Res., 10: 34-40.

Jatasra, D.S. and R.S. Paroda, 1980b. Inheritance of Kernel Weight in wheat (Triticum aestivum L.) Haryana agric. Univ. J. Res., 10: 467-471.

Jatasra, D.S. and R.S. Paroda, 1980c. Genetics of yield and components in bread wheat. Indian J. agric. Sci., 50: 379-382.

Jinks, J.L. and B.I. Hayman, 1953. The analysis of diallel crosses. Maize Genetics Newsletter 27: 48-54.

Jinks, J.L. 1954. The analysis of heritable variation in a diallel cross of Nicotiana rustica varieties. Genetics 39: 767-788.

Jinks, J.L. 1955. A survey of the genetical basis of heterosis in a variety of diallel crosses. Heridity, 9: 223-238.

Jinks, J.L. 1956. The F_2 and backcross generation from a set of diallel crosses. Heredity, 10: 1-30.

Jinks, J.L. and K. Mather. 1955. Stability in development of heterozygotes and homozygotes. Proc. Roy. Soc. B. 143: 561-578.

Jink, J.L., and J.M. Stevens, 1959. The component of variation among family means in diallel crosses. Genetics 44: 297-308.

Jinks, O.J.L. and J.M. Perkins. 1969. The detection of linked epistasis genes for a matrical trait. Heredity, 24: 465-475.

Jinks, J.L. and J.M. Perkins, 1970. A general method for the detection of additive, dominance and epistatic components of variation. III. F_2 and back cross populations. Heredity. 25: 419-429.

Joarder, O.I. and A.M. Eunus, 1968. Inheritance of earliness and plant height in an eleven parent diallel cross of *Brassica juncea* L. Sci. Res., 5: 200-211.

Joarder, O.I. and A.M. Eunus, 1977. A study of genotype-environment interaction shown by heading and harvesting time of *Brassica campestris* L. Z. Pflanzenzuchtg. 78: 310-318.

Joarder, O.I., S.K. Ghose and M. Salehuzzaman, 1978. Genotype-environment interaction shown by yield and some of its components of *Brassica campestris* L. Z. Pflanzenzuchtg. 81: 248-257.

Joarder, O.I., R. Islam, A.M. Eunus, M.A. Rashid and K.N. Rahman, 1979. Fertilizer and irrigation effects on Norteno 67 wheat. Bangladesh J. Agriculture, 4:97-101.

Joarder, O.I., M.A. Azam, Uddin, S.K. Bhadra, M.A. Khaleque and A.M. Eunus, 1980a. Genotype-environment interaction of leaf characteristics of rice associated with difference in soils. Acta. Agronomica, 28:(in press).

Joarder, O.I., M.M. Uddin, S. Rahman, M.A. Khalqque and A.M. Eunus, 1980b. Studies on root-shoot system of rice (Oryza sativa L.) in relation to genotype-environment interaction. J. Thee. Appl. Genet. (Sent for publication).

Joarder, O.I., S.N. Islam, M.M. Uddin and A.M. Eunus, 1982. Analysis of some quantitative characters from all possible reciprocal crosses between aset of parental lines of wheat. Indian J. agric. Sci., 52:(in press).

Johnson, L.P.V., and R. Aksel, 1959. Inheritance of yielding capacity in a 15-parent diallel cross of barley. Can. J. Genet. Cytol. 11: 208-265.

Kempthorne, O. 1954. The correlation between relatives in a random mating population. Proc. Roy. Soc. B. 143:103-113.

Kempthorne, O. 1956. The theory of the diallel cross. Genetics, 41: 451-459.

Kempthorne, O. and R.N. Curnow. 1961. The partial diallel cross. Biometrics, 17: 229-250.

Krishnaswami, S., M.S. Jolly and S.S. Rao, 1964. Diallel analysis of quantitative characters in multivoltine races of silkworm. Indian J. Genet. 24: 213-222.

Leighty, C.E. and W.J. Sando, 1924. The Blooming of Wheat Flowers. Journal of Agricultural Research, 27: 231-244.

Mather, K., 1949. Biometrical Genetics. First Edition. Methuen, London.

Mather, K., and R.N. Jones, 1958. Interaction of genotype and environment in continuous variation. I. Description. Biometrics 14: 343-359.

Mather, K., and J.L. Jinks, 1971. Biometrical Genetics. Second Edition, Chapman and Hall, London.

Mather, K., and J.L. Jinks, 1977. Introduction to Biometrical Genetics. First Edition, Chapman and Hall, London.

Matzinger, D.F., and O. Kempthorne, 1956. The modified diallel table with partial inbreeding and interactions with environments. Genetics, 41:822-833.

Matzinger, D.F., G.F. Sprague, and C.C. Cockerham. 1959. Diallel crosses of maize in experiments repeated over locations and years. Agron. J. 51: 346-350.

Pal, B.P. and N. Alam, 1938. The effect of certain external factors upon the manifestation of hybrid vigour in wheat. Proc. Indian Aca. Sci., 7: 109-124.

Pal, B.P., 1964. Improvement of wheat in India. Yearbook, Bharat Krishak Sarmaj, New Delhi, pp. 317-370.

Parodi, P.C., F.L. Patterson and W.E. Hyquist, 1970. A six-parent diallel cross analysis of coleoptile elongation in wheat (Triticum aestivum L.) Crop. Sci. 10: 587-90.

Paroda, R.S. and A.B. Joshi, 1970a. Genetic architecture of yield and components of yield in wheat. Indian J. Genet. Pl. Breed., 30: 298-314.

Paroda, R.S. and A.B. Joshi, 1970b. Combining ability in wheat. Indian J. Genet Pl. Breed., 30: 630-637.

Paroda, R.S. and J.D. Hayes, 1971. An investigation of genotype-environment interactions for rate of ear emergence in spring barley. Heredity, 26: 157-175.

Patanothai, A., and R.E. Atkins, 1974. Genetic effects for mean yield and yield responses to environments in three way and single cross hybrids of grain sarghum. Crop. Sci. 14: 485-488.

Paul, N.K., O.I. Joarder, and A.M. Eunus, 1976. Variation of yield and some of its traits in eight crosses of local and Indian rape varieties. J. Asiatic Soc. Bang. 2: 31-41.

Percival, John. 1921. The wheat plant. Duckworth and Co. London. 463 p. illns.

Perkins, J.M. and J.L. Jinks., 1968a. Environmental and genotype-environmental components of variability. III. Multiple lines and crosses. Heredity, 23: 339-356.

Perkins, J.M. and J.L. Jinks., 1968b. Environmental and genotype-environmental components of variability. IV. Non-Linear interaction for multiple inbred lines. Heredity, 23: 525-535.

Perkins, J.M. 1970. Environmental and genotype-environmental components of variability. VI. Diallel sets of crosses, Heredity, 25: 29-40.

Perkins, J.M. and J.L. Jinks., 1973. The assessment and specificity of environmental and genotype-environmental components of variability. Heredity, 30(2), 111-126.

Petr, F.C. and K.J. Frey, 1966. Genotypic correlations, dominance and heritability of quantitative characters in Oal. Crop Sci., 6: 259-262.

Porceddu, E., G.T. Scarascia-Mugnozza. 1974. Seedling growth characteristics in varieties, mutant lines and crosses of durum wheat. IAEA- PL. - 503/35, 261-273 /8 ref./ Laboratorio del Germoplasma, CNR, Bari, Italy.

Powers, L. 1951. Gene analysis by the partitioning methods when interaction of gene are involved. Bot. Gaz. 113+1-23

Quisenberry, K.S. 1931. Inheritance of winter hardiness, growth habit and stem rust reaction in crosses between Minhardi winter and H-44 spring wheats. USDA Tech. Bull. 218, 45pp.

Rajas, B.A., and G.F. Sprague, 1952. A comparison of variance components in corn yield traits. III. General and specific combining ability and their interaction with locations and years. Agron. J. 44: 462-466.

Robinson, H.F. and R.E. Comstock, 1955. Analysis of genetic variability in corn with reference to probable effects of selection. Cold Spring Harbour Symp. on quantitative Biol. 20: 127-136.

Row, P.B. and R.A. Andrew, 1964. Phenotypic stability for a systematic series of corn genotypes. Crop Sci., 4: 563-564.

Roy, N.N., Yadav, S.P. and Ram J. 1970. Influence of temperature on the growth of wheat coleoptile. Indian J. agric. Sci. 40: 948-53.

Scarle, S.R., 1966. Metrix Algebra for Biologists. Wiley, N.Y.

Scarascia G.T., Mugnozza, and E. Porceddu. 1975. Genetic studies of coleoptile length in Triticum durum. pp. 301-8. Inst. Pl. Br. Univ. Bari., Italy.

Schmidt, J. 1919. Diallel crossing with tront. J. Genetics 9: 61-67.

Sharma, G.S. and R.B. Singh, 1976. Inheritance of plant height and spike length in dwarf spring wheat. Indian J. Genet. Pl. Breed., 30: 173-183.

Sharma, G.S. Rachana Paliwal and R.B. Singh, 1982. Interrelationship between coleoptile length, seedling height, culm length, yield and their traits in wheat. Indian J. Genet., 42:172-175.

Singh, K.B. and V.P. Gupta, 1969. Combining ability in wheat. Indian J. Genet. Pl. Breed., 29:227-232.

Spearman, G. 1904. The proof and measurement of association between two things. Amer. J. Psych., 15, 72-101.

Sprague, G.F. and L.A. Tatum. 1942. General versus specific combining ability in single crosses of corn. J. Amer. Soc. Agron. 34: 923-932.

Sunderman, D.W., 1963. Seedling emergence of winter wheats and its association with depth of sowing, coleoptile length under various conditions and plant height Agron J. 56: 23-25.

Sun, P.L.F., H.L. Shands and R.A. Forsbery, 1972. Inheritance of kernel weight in six spring wheat crosses. crop. Sci., 12: 1-5.

Sengupta, K., R.K. Datta and S.N. Biswas, 1974. Effect of multiple crossing on the population pattern of the progeny in silkworms. Indian J. Genet. 34: 241-248.

Singh, K.B. and V.P. Gupta, 1969. Combining ability in wheat. Indian J. Genet Pl. Breed., 29: 227-232.

Tandon, J.P., A.B. Joshi and K.B.L. Janin, 1970. Comparison of graphic and combining ability analysis of diallel crosses in wheat. Indian J. Genet. Pl. Breed.,30:91-103.

Verma, M.M. and K.S. Gill, 1975. Genotype-environment interaction - its measurement and significance in plant breeding. Teaching Aid Bul. No. 01:1-40.

Virk, D.S.; G.S. Bhullar; K.S. Gill; G.S. Ponni, 1977. Genetics of coleoptile measurements in three breed wheat crosses. Cereal Research Communications. 5(4) 419-430 /En, 6 rep./ Dep. Genet., Univ. Birmingham, U.K.

Walton, P.D., 1968. Spring wheat variety trials in the praire provinces. Can. J. Plant Sci., 48:601-609.

Walton, P.D. 1969. Inheritance of morphological characters associated with yield in spring wheat. Can. J. Plant Sci. 49: 587-596.

Walton, P.D. 1971a. Heterosis in spring wheat. Crop. Sci. 11: 422-424.

Walton, P.D. 1971b. The genetics of yield in spring wheat. Can. J. Genet. Cylol. 13: 110-114.

Walton, P.D. 1971c. The use of factor analysis in determining characters for yield selection in wheat. Euphytica 20.

Walton, P.D. 1972. Quantitative inheritance of yield and associated factors in spring wheat. Euphytica, 21: 553-556.

Whan, B.R. 1976. The association between coleoptile length in semidwarf and standard wheats. Journal of the Australian Institute of Agricultural Science. 42(3) 194-196 /En, 11 ref./ . Dep. Agric. State Res. Farm, Werribee, Vic., Australia.

Whan, B.R. 1976. The emergence of semidwarf and standard wheats, and its association with coleoptile length. Australian Journal of Experimental Agriculture Dep. Agric., Werribee, Victoria, Australia.

Whitehouse, R.N.H., J.B. Thompson, and N.A.M.V. Ribeiro. 1958. Studies on the breeding of self pollinated cereals. II. The use of diallel cross analysis in yield prediction. Euphytica, 7: 147-169.

Westerman, J.M. 1971a. Genotype-environment interaction and developmental regulation in *Arabidopsis thaliana*. III. Inbred lines; analysis. Heredity, 26: 93-106.

Westerman, J.M. 1971b. Genotype-environment interaction and development regulation in *Arabidopsis thaliana*. III. Inbred lines, analysis of response to photoperiod. Heredity, 26: 373-382.

Yadev, S.P. and B.R. Murty, 1976. Heterosis and combining ability in crosses of different height categories in bread wheat. Indian J. Genet. Pl. Breed., 36: 184-196.

Yates, F. and W.G. Cochran, 1938. The analysis of groups of experiment. J. Agric. Sci., 28: 556-580.

Yates, F. 1947. Analysis of data from all possible reciprocal crosses between a set of parental lines. Heredity 1: 287-301.